

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property
Organization
International Bureau



(43) International Publication Date
25 March 2004 (25.03.2004)

PCT

(10) International Publication Number
WO 2004/024888 A2

-
- (51) International Patent Classification⁷: C12N Madera Avenue, San Carlos, CA 94070 (US). **ZHANG, HaiGuang** [US/US]; 4833 El Grande Place, El Sobrante, CA 94803 (US).
- (21) International Application Number: PCT/US2003/029056
- (22) International Filing Date: 15 September 2003 (15.09.2003)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data: 60/411,152 16 September 2002 (16.09.2002) US
- (71) Applicant (*for all designated States except US*): EX-ELIXIS, INC. [US/US]; P.O. Box 511, 170 Harbor Way, South San Francisco, CA 94083-0511 (US).
- (72) Inventors; and
- (75) Inventors/Applicants (*for US only*): FRANCIS-LANG, Helen [GB/US]; 1782 Pacific Avenue #2, San Francisco, CA 94109 (US). FRIEDMAN, Lori [US/US]; 113 Arundel Road, San Carlos, CA 94070 (US). KIDD, Thomas [GB/US]; 643 Lake Street, San Francisco, CA 94118 (US). ROCHE, Siobhan [IE/IE]; 30 Moatfield Park, Coolock, Dublin 5 (IE). BELVIN, Marcia [US/US]; 921 Santa Fe Avenue, Albany, CA 94706 (US). PLOWMAN, Gregory, D. [US/US]; 35 Winding Way, San Carlos, CA 94070 (US). KARIM, Felix, D. [US/US]; 732 Laurel Drive, Walnut Creek, CA 94596 (US). KEYES, Linda, N. [US/US]; 46
- (74) Agents: SHAYESTEH, Laleh et al.; Exelixis, Inc., P.O.Box 511, 170 Harbor Way, South San Francisco, CA 94083-0511 (US).
- (81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.
- (84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 2004/024888 A2

(54) Title: WNHs AS MODIFIERS OF p53, p21, AND BRANCHING MORPHOGENESIS PATHWAYS AND METHODS OF USE

(57) Abstract: Human WHN genes are identified as modulators of the p21, p53, or branching morphogenesis pathway, and thus are therapeutic targets for disorders associated with defective p21, p53, or branching morphogenesis function. Methods for identifying modulators of p21, p53, or branching morphogenesis, comprising screening for agents that modulate the activity of WHN are provided.

**WHNs AS MODIFIERS OF p53, p21, AND BRANCHING MORPHOGENESIS
PATHWAYS AND METHODS OF USE**

REFERENCE TO RELATED APPLICATIONS

5 This application claims priority to U.S. provisional patent application 60/411,152 filed 9/16/2002. The contents of the prior applications are hereby incorporated in their entirety.

BACKGROUND OF THE INVENTION

10 The p53 gene is mutated in over 50 different types of human cancers, including familial and spontaneous cancers, and is believed to be the most commonly mutated gene in human cancer (Zambetti and Levine, FASEB (1993) 7:855-865; Hollstein, *et al.*, Nucleic Acids Res. (1994) 22:3551-3555). Greater than 90% of mutations in the p53 gene are missense mutations that alter a single amino acid that inactivates p53 function.
15 Aberrant forms of human p53 are associated with poor prognosis, more aggressive tumors, metastasis, and short survival rates (Mitsudomi *et al.*, Clin Cancer Res 2000 Oct; 6(10):4055-63; Koshland, Science (1993) 262:1953).

The human p53 protein normally functions as a central integrator of signals including DNA damage, hypoxia, nucleotide deprivation, and oncogene activation (Prives, Cell (1998) 95:5-8). In response to these signals, p53 protein levels are greatly increased with the result that the accumulated p53 activates cell cycle arrest or apoptosis depending on the nature and strength of these signals. Indeed, multiple lines of experimental evidence have pointed to a key role for p53 as a tumor suppressor (Levine, Cell (1997) 88:323-331). For example, homozygous p53 "knockout" mice are developmentally normal but exhibit nearly 100% incidence of neoplasia in the first year of life (Donehower *et al.*, Nature (1992) 356:215-221).

The biochemical mechanisms and pathways through which p53 functions in normal and cancerous cells are not fully understood, but one clearly important aspect of p53 function is its activity as a gene-specific transcriptional activator. Among the genes with known p53-response elements are several with well-characterized roles in either regulation of the cell cycle or apoptosis, including GADD45, p21/Waf1/Cip1, cyclin G, Bax, IGF-BP3, and MDM2 (Levine, Cell (1997) 88:323-331).

The p21/CDKN1/WAF1/CIP1 protein (El-Deiry, W. S.; *et al.* Cell 75: 817-825, 1993; Harper, J. W.; *et al.* Cell 75: 805-816, 1993; Huppi, Ket al. Oncogene 9: 3017-3020, 1994) is a cell cycle control protein that inhibits cyclin-kinase activity, is tightly regulated

at the transcriptional level by p53, and mediates p53 suppression of tumor cell growth. Along with p53, p21 appears to be essential for maintaining the G2 checkpoint in human cells (Bunz, F.; Dutriaux, A.; et al. *Science* 282:1497-1501, 1998). Sequences of P21 are well-conserved throughout evolution, and have been identified in species as diverse as
5 human (Genbank Identifier 13643057), *Drosophila melanogaster* (GI# 1684911),
Caenorhabditis elegans (GI#4966283), and yeast (GI#2656016).

Several essential organs (e.g., lungs, kidney, lymphatic system and vasculature) are made up of complex networks of tube-like structures that serve to transport and exchange fluids, gases, nutrients and waste. The formation of these complex branched networks
10 occurs by the evolutionarily conserved process of branching morphogenesis, in which successive ramification occurs by sprouting, pruning and remodeling of the network. During human embryogenesis, blood vessels develop via two processes: vasculogenesis, whereby endothelial cells are born from progenitor cell types; and angiogenesis, in which new capillaries sprout from existing vessels.

15 Branching morphogenesis encompasses many cellular processes, including proliferation, survival/apoptosis, migration, invasion, adhesion, aggregation and matrix remodeling. Numerous cell types contribute to branching morphogenesis, including endothelial, epithelial and smooth muscle cells, and monocytes. Gene pathways that modulate the branching process function both within the branching tissues as well as in
20 other cells, e.g., certain monocytes can promote an angiogenic response even though they may not directly participate in the formation of the branch structures.

An increased level of angiogenesis is central to several human disease pathologies, including rheumatoid arthritis and diabetic retinopathy, and, significantly, to the growth, maintenance and metastasis of solid tumors (for detailed reviews see Liotta LA et al, 1991
25 Cell 64:327-336; Folkman J., 1995 Nature Medicine 1:27-31; Hanahan D and Folkman J., 1996 Cell 86:353-364). Impaired angiogenesis figures prominently in other human diseases, including heart disease, stroke, infertility, ulcers and scleroderma.

The transition from dormant to active blood vessel formation involves modulating the balance between angiogenic stimulators and inhibitors. Under certain pathological
30 circumstances an imbalance arises between local inhibitory controls and angiogenic inducers resulting in excessive angiogenesis, while under other pathological conditions an imbalance leads to insufficient angiogenesis. This delicate equilibrium of pro- and anti-angiogenic factors is regulated by a complex interaction between the extracellular matrix, endothelial cells, smooth muscle cells, and various other cell types, as well as

environmental factors such as oxygen demand within tissues. The lack of oxygen (hypoxia) in and around wounds and solid tumors is thought to provide a key driving force for angiogenesis by regulating a number of angiogenic factors, including Hypoxia Induced Factor alpha (HIF1 alpha) (Richard DE et al., Biochem Biophys Res Commun. 1999 Dec 5 29;266(3):718-22). HIF1 in turn regulates expression of a number of growth factors including Vascular Endothelial Growth Factor (VEGF) (Connolly DT, J Cell Biochem 1991 Nov;47(3):219-23). Various VEGF ligands and receptors are vital regulators of endothelial cell proliferation, survival, vessel permeability and sprouting, and lymphangiogenesis (Neufeld G et al., FASEB J 1999 Jan;13(1):9-22; Stacker SA et al., 10 Nature Medicine 2001 7:186-191; Skobe M, et al., Nature Medicine 2001 7:192-198; Makinen T, et al., Nature Medicine 2001 7:199-205).

Most known angiogenesis genes, their biochemical activities, and their organization into signaling pathways are employed in a similar fashion during angiogenesis in human, mouse and Zebrafish, as well as during branching morphogenesis 15 of the *Drosophila* trachea. Accordingly, *Drosophila* tracheal development and zebrafish vascular development provide useful models for studying mammalian angiogenesis (Sutherland D et al., Cell 1996, 87:1091-101; Roush W, Science 1996, 274:2011; Skaer H., Curr Biol 1997, 7:R238-41; Metzger RJ, Krasnow MA. Science. 1999. 284:1635-9; Roman BL, and Weinstein BM. Bioessays 2000, 22:882-93).

20 WHN (winged helix nude) is a member of the winged helix domain family of transcription factors. WHN is the human homolog of the Whn gene in the mouse and the rat, which disrupt normal hair growth and thymus development, causing nude mice and rats to be immune-deficient (Nehls et al (1994) Nature 372: 103-107). Mutations in winged-helix domain genes cause homeotic transformations in *Drosophila* and distort cell-fate decisions during vulval development in *C. elegans*.

25 FOXN4 is a forkhead/winged helix family member that is expressed during neural development in the retina, the ventral hindbrain and spinal cord and dorsal midbrain, and may play a role in ocular retardation(Gouge A et al (2001) Mech Dev. 107:203-6).

The ability to manipulate the genomes of model organisms such as *Drosophila* 30 provides a powerful means to analyze biochemical processes that, due to significant evolutionary conservation, have direct relevance to more complex vertebrate organisms. Due to a high level of gene and pathway conservation, the strong similarity of cellular processes, and the functional conservation of genes between these model organisms and mammals, identification of the involvement of novel genes in particular pathways and

their functions in such model organisms can directly contribute to the understanding of the correlative pathways and methods of modulating them in mammals (see, for example, Mechler BM et al., 1985 EMBO J 4:1551-1557; Gateff E. 1982 Adv. Cancer Res. 37: 33-74; Watson KL., et al., 1994 J Cell Sci. 18: 19-33; Miklos GL, and Rubin GM. 1996 Cell 86:521-529; Wassarman DA, et al., 1995 Curr Opin Gen Dev 5: 44-50; and Booth DR. 1999 Cancer Metastasis Rev. 18: 261-284). For example, a genetic screen can be carried out in an invertebrate model organism having underexpression (e.g. knockout) or overexpression of a gene (referred to as a "genetic entry point") that yields a visible phenotype. Additional genes are mutated in a random or targeted manner. When a gene mutation changes the original phenotype caused by the mutation in the genetic entry point, the gene is identified as a "modifier" involved in the same or overlapping pathway as the genetic entry point. When the genetic entry point is an ortholog of a human gene implicated in a disease pathway, such as p53, modifier genes can be identified that may be attractive candidate targets for novel therapeutics.

All references cited herein, including patents, patent applications, publications, and sequence information in referenced Genbank identifier numbers, are incorporated herein in their entireties.

SUMMARY OF THE INVENTION

We have discovered genes that modify the p21, p53, or branching morphogenesis pathway in *Drosophila*, and identified their human orthologs, hereinafter referred to as WHN (Winged helix nude). The invention provides methods for utilizing these p21, p53, or branching morphogenesis modifier genes and polypeptides to identify WHN-modulating agents that are candidate therapeutic agents that can be used in the treatment of disorders associated with defective or impaired p21, p53, or branching morphogenesis function and/or WHN function. Preferred WHN-modulating agents specifically bind to WHN polypeptides and restore p21, p53, or branching morphogenesis function. Other preferred WHN-modulating agents are nucleic acid modulators such as antisense oligomers and RNAi that repress WHN gene expression or product activity by, for example, binding to and inhibiting the respective nucleic acid (i.e. DNA or mRNA).

WHN modulating agents may be evaluated by any convenient *in vitro* or *in vivo* assay for molecular interaction with a WHN polypeptide or nucleic acid. In one embodiment, candidate WHN modulating agents are tested with an assay system comprising a WHN polypeptide or nucleic acid. Agents that produce a change in the

activity of the assay system relative to controls are identified as candidate p21, p53, or branching morphogenesis modulating agents. The assay system may be cell-based or cell-free. WHN-modulating agents include WHN related proteins (e.g. dominant negative mutants, and biotherapeutics); WHN-specific antibodies; WHN-specific antisense oligomers and other nucleic acid modulators; and chemical agents that specifically bind to or interact with WHN or compete with WHN binding partner (e.g. by binding to a WHN binding partner). In one specific embodiment, a small molecule modulator is identified using a binding assay. In specific embodiments, the screening assay system is selected from a binding assay, an apoptosis assay, a cell proliferation assay, an angiogenesis assay, a cell migration assay, a tubulogenesis assay, cell adhesion assay, a sprouting assay, and a hypoxic induction assay.

In another embodiment, candidate p21, p53, or branching morphogenesis pathway modulating agents are further tested using a second assay system that detects changes in the p21, p53, or branching morphogenesis pathway, such as angiogenic, apoptotic, or cell proliferation changes produced by the originally identified candidate agent or an agent derived from the original agent. The second assay system may use cultured cells or non-human animals. In specific embodiments, the secondary assay system uses non-human animals, including animals predetermined to have a disease or disorder implicating the p21, p53, or branching morphogenesis pathway, such as an angiogenic, apoptotic, or cell proliferation disorder (e.g. cancer).

The invention further provides methods for modulating the WHN function and/or the p21, p53, or branching morphogenesis pathway in a mammalian cell by contacting the mammalian cell with an agent that specifically binds a WHN polypeptide or nucleic acid. The agent may be a small molecule modulator, a nucleic acid modulator, or an antibody and may be administered to a mammalian animal predetermined to have a pathology associated the p21, p53, or branching morphogenesis pathway.

DETAILED DESCRIPTION OF THE INVENTION

Genetic screens were designed to identify modifiers of the p21, p53, or branching morphogenesis pathways in *Drosophila*. Modifiers of the p21, p53, or branching morphogenesis pathway were identified. Accordingly, vertebrate orthologs of these modifiers, and preferably the human orthologs, WHN genes (i.e., nucleic acids and polypeptides) are attractive drug targets for the treatment of pathologies associated with a

defective p21, p53, or branching morphogenesis signaling pathways, such as cancer.

Table 1 lists the modifiers and their orthologs.

In vitro and in vivo methods of assessing WHN function are provided herein.

Modulation of the WHN or their respective binding partners is useful for understanding

5 the association of the p21, p53, or branching morphogenesis pathway and its members in normal and disease conditions and for developing diagnostics and therapeutic modalities for p21, p53, or branching morphogenesis related pathologies. WHN-modulating agents that act by inhibiting or enhancing WHN expression, directly or indirectly, for example, by affecting a WHN function such as enzymatic (e.g., catalytic) or binding activity, can be
10 identified using methods provided herein. WHN modulating agents are useful in diagnosis, therapy and pharmaceutical development.

As used herein, branching morphogenesis encompasses the numerous cellular process involved in the formation of branched networks, including proliferation, survival/apoptosis, migration, invasion, adhesion, aggregation and matrix remodeling. As
15 used herein, pathologies associated with branching morphogenesis encompass pathologies where branching morphogenesis contributes to maintaining the healthy state, as well as pathologies whose course may be altered by modulation of the branching morphogenesis.

Nucleic acids and polypeptides of the invention

20 Sequences related to WHN nucleic acids and polypeptides that can be used in the invention are disclosed in Genbank (referenced by Genbank identifier (GI) or RefSeq number), and shown in Table 1.

The term "WHN polypeptide" refers to a full-length WHN protein or a functionally active fragment or derivative thereof. A "functionally active" WHN fragment
25 or derivative exhibits one or more functional activities associated with a full-length, wild-type WHN protein, such as antigenic or immunogenic activity, ability to bind natural cellular substrates, etc. The functional activity of WHN proteins, derivatives and fragments can be assayed by various methods known to one skilled in the art (Current Protocols in Protein Science (1998) Coligan *et al.*, eds., John Wiley & Sons, Inc.,
30 Somerset, New Jersey) and as further discussed below. In one embodiment, a functionally active WHN polypeptide is a WHN derivative capable of rescuing defective endogenous WHN activity, such as in cell based or animal assays; the rescuing derivative may be from the same or a different species. For purposes herein, functionally active fragments also include those fragments that comprise one or more structural domains of a WHN, such as

a binding domain. Protein domains can be identified using the PFAM program (Bateman A., et al., Nucleic Acids Res, 1999, 27:260-2). Methods for obtaining WHN polypeptides are also further described below. In some embodiments, preferred fragments are functionally active, domain-containing fragments comprising at least 25 contiguous amino acids, preferably at least 50, more preferably 75, and most preferably at least 100 contiguous amino acids of a WHN. In further preferred embodiments, the fragment comprises the entire functionally active domain.

The term "WHN nucleic acid" refers to a DNA or RNA molecule that encodes a WHN polypeptide. Preferably, the WHN polypeptide or nucleic acid or fragment thereof is from a human, but can also be an ortholog, or derivative thereof with at least 70% sequence identity, preferably at least 80%, more preferably 85%, still more preferably 90%, and most preferably at least 95% sequence identity with human WHN. Methods of identifying orthologs are known in the art. Normally, orthologs in different species retain the same function, due to presence of one or more protein motifs and/or 3-dimensional structures. Orthologs are generally identified by sequence homology analysis, such as BLAST analysis, usually using protein bait sequences. Sequences are assigned as a potential ortholog if the best hit sequence from the forward BLAST result retrieves the original query sequence in the reverse BLAST (Huynen MA and Bork P, Proc Natl Acad Sci (1998) 95:5849-5856; Huynen MA et al., Genome Research (2000) 10:1204-1210).

Programs for multiple sequence alignment, such as CLUSTAL (Thompson JD et al, 1994, Nucleic Acids Res 22:4673-4680) may be used to highlight conserved regions and/or residues of orthologous proteins and to generate phylogenetic trees. In a phylogenetic tree representing multiple homologous sequences from diverse species (e.g., retrieved through BLAST analysis), orthologous sequences from two species generally appear closest on the tree with respect to all other sequences from these two species. Structural threading or other analysis of protein folding (e.g., using software by ProCeryon, Biosciences, Salzburg, Austria) may also identify potential orthologs. In evolution, when a gene duplication event follows speciation, a single gene in one species, such as *Drosophila*, may correspond to multiple genes (paralogs) in another, such as human. As used herein, the term "orthologs" encompasses paralogs. As used herein, "percent (%) sequence identity" with respect to a subject sequence, or a specified portion of a subject sequence, is defined as the percentage of nucleotides or amino acids in the candidate derivative sequence identical with the nucleotides or amino acids in the subject sequence (or specified portion thereof), after aligning the sequences and introducing gaps, if necessary

to achieve the maximum percent sequence identity, as generated by the program WU-BLAST-2.0a19 (Altschul *et al.*, J. Mol. Biol. (1997) 215:403-410) with all the search parameters set to default values. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched. A % identity value is determined by the number of matching identical nucleotides or amino acids divided by the sequence length for which the percent identity is being reported. "Percent (%) amino acid sequence similarity" is determined by doing the same calculation as for determining % amino acid sequence identity, but including conservative amino acid substitutions in addition to identical amino acids in the computation.

A conservative amino acid substitution is one in which an amino acid is substituted for another amino acid having similar properties such that the folding or activity of the protein is not significantly affected. Aromatic amino acids that can be substituted for each other are phenylalanine, tryptophan, and tyrosine; interchangeable hydrophobic amino acids are leucine, isoleucine, methionine, and valine; interchangeable polar amino acids are glutamine and asparagine; interchangeable basic amino acids are arginine, lysine and histidine; interchangeable acidic amino acids are aspartic acid and glutamic acid; and interchangeable small amino acids are alanine, serine, threonine, cysteine and glycine.

Alternatively, an alignment for nucleic acid sequences is provided by the local homology algorithm of Smith and Waterman (Smith and Waterman, 1981, Advances in Applied Mathematics 2:482-489; database: European Bioinformatics Institute; Smith and Waterman, 1981, J. of Molec.Biol., 147:195-197; Nicholas *et al.*, 1998, "A Tutorial on Searching Sequence Databases and Sequence Scoring Methods" (www.psc.edu) and references cited therein.; W.R. Pearson, 1991, Genomics 11:635-650). This algorithm can be applied to amino acid sequences by using the scoring matrix developed by Dayhoff (Dayhoff: Atlas of Protein Sequences and Structure, M. O. Dayhoff ed., 5 suppl. 3:353-358, National Biomedical Research Foundation, Washington, D.C., USA), and normalized by Gribskov (Gribskov 1986 Nucl. Acids Res. 14(6):6745-6763). The Smith-Waterman algorithm may be employed where default parameters are used for scoring (for example, gap open penalty of 12, gap extension penalty of two). From the data generated, the "Match" value reflects "sequence identity."

Derivative nucleic acid molecules of the subject nucleic acid molecules include sequences that hybridize to the nucleic acid sequence of a WHN. The stringency of

hybridization can be controlled by temperature, ionic strength, pH, and the presence of denaturing agents such as formamide during hybridization and washing. Conditions routinely used are set out in readily available procedure texts (*e.g.*, Current Protocol in Molecular Biology, Vol. 1, Chap. 2.10, John Wiley & Sons, Publishers (1994); Sambrook *et al.*, Molecular Cloning, Cold Spring Harbor (1989)). In some embodiments, a nucleic acid molecule of the invention is capable of hybridizing to a nucleic acid molecule containing the nucleotide sequence of a WHN under stringent hybridization conditions that comprise: prehybridization of filters containing nucleic acid for 8 hours to overnight at 65° C in a solution comprising 6X single strength citrate (SSC) (1X SSC is 0.15 M NaCl, 0.015 M Na citrate; pH 7.0), 5X Denhardt's solution, 0.05% sodium pyrophosphate and 100 µg/ml herring sperm DNA; hybridization for 18-20 hours at 65° C in a solution containing 6X SSC, 1X Denhardt's solution, 100 µg/ml yeast tRNA and 0.05% sodium pyrophosphate; and washing of filters at 65° C for 1h in a solution containing 0.2X SSC and 0.1% SDS (sodium dodecyl sulfate).

In other embodiments, moderately stringent hybridization conditions are used that comprise: pretreatment of filters containing nucleic acid for 6 h at 40° C in a solution containing 35% formamide, 5X SSC, 50 mM Tris-HCl (pH7.5), 5mM EDTA, 0.1% PVP, 0.1% Ficoll, 1% BSA, and 500 µg/ml denatured salmon sperm DNA; hybridization for 18-20h at 40° C in a solution containing 35% formamide, 5X SSC, 50 mM Tris-HCl (pH7.5), 5mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 µg/ml salmon sperm DNA, and 10% (wt/vol) dextran sulfate; followed by washing twice for 1 hour at 55° C in a solution containing 2X SSC and 0.1% SDS.

Alternatively, low stringency conditions can be used that comprise: incubation for 8 hours to overnight at 37° C in a solution comprising 20% formamide, 5 x SSC, 50 mM sodium phosphate (pH 7.6), 5X Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured sheared salmon sperm DNA; hybridization in the same buffer for 18 to 20 hours; and washing of filters in 1 x SSC at about 37° C for 1 hour.

Isolation, Production, Expression, and Mis-expression of WHN Nucleic Acids and Polypeptides

WHN nucleic acids and polypeptides, useful for identifying and testing agents that modulate WHN function and for other applications related to the involvement of WHN in the p21, p53, or branching morphogenesis pathways. WHN nucleic acids and derivatives and orthologs thereof may be obtained using any available method. For instance,

techniques for isolating cDNA or genomic DNA sequences of interest by screening DNA libraries or by using polymerase chain reaction (PCR) are well known in the art. In general, the particular use for the protein will dictate the particulars of expression, production, and purification methods. For instance, production of proteins for use in screening for modulating agents may require methods that preserve specific biological activities of these proteins, whereas production of proteins for antibody generation may require structural integrity of particular epitopes. Expression of proteins to be purified for screening or antibody production may require the addition of specific tags (*e.g.*, generation of fusion proteins). Overexpression of a WHN protein for assays used to assess WHN function, such as involvement in cell cycle regulation or hypoxic response, may require expression in eukaryotic cell lines capable of these cellular activities. Techniques for the expression, production, and purification of proteins are well known in the art; any suitable means therefore may be used (*e.g.*, Higgins SJ and Hames BD (eds.) *Protein Expression: A Practical Approach*, Oxford University Press Inc., New York 1999; Stanbury PF et al., 10 *Principles of Fermentation Technology*, 2nd edition, Elsevier Science, New York, 1995; Doonan S (ed.) *Protein Purification Protocols*, Humana Press, New Jersey, 1996; Coligan JE et al, *Current Protocols in Protein Science* (eds.), 1999, John Wiley & Sons, New York). In particular embodiments, recombinant WHN is expressed in a cell line known to have defective p53 or p21 function (*e.g.* SAOS-2 osteoblasts, H1299 lung cancer cells, 15 C33A and HT3 cervical cancer cells, HT-29 and DLD-1 colon cancer cells, and HCT116 colon cancer cells, among others, available from American Type Culture Collection (ATCC), Manassas, VA). The recombinant cells are used in cell-based screening assay systems of the invention, as described further below.

The nucleotide sequence encoding a WHN polypeptide can be inserted into any appropriate expression vector. The necessary transcriptional and translational signals, including promoter/enhancer element, can derive from the native WHN gene and/or its flanking regions or can be heterologous. A variety of host-vector expression systems may be utilized, such as mammalian cell systems infected with virus (*e.g.* vaccinia virus, adenovirus, *etc.*); insect cell systems infected with virus (*e.g.* baculovirus); 20 microorganisms such as yeast containing yeast vectors, or bacteria transformed with bacteriophage, plasmid, or cosmid DNA. A host cell strain that modulates the expression of, modifies, and/or specifically processes the gene product may be used.

To detect expression of the WHN gene product, the expression vector can comprise a promoter operably linked to a WHN gene nucleic acid, one or more origins of

replication, and, one or more selectable markers (*e.g.* thymidine kinase activity, resistance to antibiotics, *etc.*). Alternatively, recombinant expression vectors can be identified by assaying for the expression of the WHN gene product based on the physical or functional properties of the WHN protein in *in vitro* assay systems (*e.g.* immunoassays).

5 The WHN protein, fragment, or derivative may be optionally expressed as a fusion, or chimeric protein product (*i.e.* it is joined via a peptide bond to a heterologous protein sequence of a different protein), for example to facilitate purification or detection. A chimeric product can be made by ligating the appropriate nucleic acid sequences encoding the desired amino acid sequences to each other using standard methods and expressing the
10 chimeric product. A chimeric product may also be made by protein synthetic techniques, *e.g.* by use of a peptide synthesizer (Hunkapiller *et al.*, *Nature* (1984) 310:105-111).

15 Once a recombinant cell that expresses the WHN gene sequence is identified, the gene product can be isolated and purified using standard methods (*e.g.* ion exchange, affinity, and gel exclusion chromatography; centrifugation; differential solubility; electrophoresis). Alternatively, native WHN proteins can be purified from natural sources, by standard methods (*e.g.* immunoaffinity purification). Once a protein is obtained, it may be quantified and its activity measured by appropriate methods, such as immunoassay, bioassay, or other measurements of physical properties, such as crystallography.

20 The methods of this invention may also use cells that have been engineered for altered expression (mis-expression) of WHN or other genes associated with the p21, p53, or branching morphogenesis pathways. As used herein, mis-expression encompasses ectopic expression, over-expression, under-expression, and non-expression (*e.g.* by gene knock-out or blocking expression that would otherwise normally occur).

25

Genetically modified animals

30 Animal models that have been genetically modified to alter WHN expression may be used in *in vivo* assays to test for activity of a candidate p21, p53, or branching morphogenesis modulating agent, or to further assess the role of WHN in a p21, p53, or branching morphogenesis pathway process such as apoptosis or cell proliferation. Preferably, the altered WHN expression results in a detectable phenotype, such as decreased or increased levels of cell proliferation, angiogenesis, or apoptosis compared to control animals having normal WHN expression. The genetically modified animal may additionally have altered p21, p53, or branching morphogenesis expression (*e.g.* p21, p53

knockout). Preferred genetically modified animals are mammals such as primates, rodents (preferably mice or rats), among others. Preferred non-mammalian species include zebrafish, *C. elegans*, and *Drosophila*. Preferred genetically modified animals are transgenic animals having a heterologous nucleic acid sequence present as an

5 extrachromosomal element in a portion of its cells, i.e. mosaic animals (see, for example, techniques described by Jakobovits, 1994, *Curr. Biol.* 4:761-763.) or stably integrated into its germ line DNA (i.e., in the genomic sequence of most or all of its cells). Heterologous nucleic acid is introduced into the germ line of such transgenic animals by genetic manipulation of, for example, embryos or embryonic stem cells of the host animal.

10 Methods of making transgenic animals are well-known in the art (for transgenic mice see Brinster et al., *Proc. Nat. Acad. Sci. USA* 82: 4438-4442 (1985), U.S. Pat. Nos. 4,736,866 and 4,870,009, both by Leder et al., U.S. Pat. No. 4,873,191 by Wagner et al., and Hogan, B., *Manipulating the Mouse Embryo*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., (1986); for particle bombardment see U.S. Pat. No., 4,945,050,

15 by Sandford et al.; for transgenic *Drosophila* see Rubin and Spradling, *Science* (1982) 218:348-53 and U.S. Pat. No. 4,670,388; for transgenic insects see Berghammer A.J. et al., *A Universal Marker for Transgenic Insects* (1999) *Nature* 402:370-371; for transgenic Zebrafish see Lin S., *Transgenic Zebrafish*, *Methods Mol Biol.* (2000);136:375-3830); for microinjection procedures for fish, amphibian eggs and birds see Houdebine and

20 Chourrout, *Experientia* (1991) 47:897-905; for transgenic rats see Hammer et al., *Cell* (1990) 63:1099-1112; and for culturing of embryonic stem (ES) cells and the subsequent production of transgenic animals by the introduction of DNA into ES cells using methods such as electroporation, calcium phosphate/DNA precipitation and direct injection see, e.g., *Teratocarcinomas and Embryonic Stem Cells, A Practical Approach*, E. J. Robertson, 25 ed., IRL Press (1987)). Clones of the nonhuman transgenic animals can be produced according to available methods (see Wilmut, I. et al. (1997) *Nature* 385:810-813; and PCT International Publication Nos. WO 97/07668 and WO 97/07669).

In one embodiment, the transgenic animal is a "knock-out" animal having a heterozygous or homozygous alteration in the sequence of an endogenous WHN gene that 30 results in a decrease of WHN function, preferably such that WHN expression is undetectable or insignificant. Knock-out animals are typically generated by homologous recombination with a vector comprising a transgene having at least a portion of the gene to be knocked out. Typically a deletion, addition or substitution has been introduced into the transgene to functionally disrupt it. The transgene can be a human gene (e.g., from a

human genomic clone) but more preferably is an ortholog of the human gene derived from the transgenic host species. For example, a mouse WHN gene is used to construct a homologous recombination vector suitable for altering an endogenous WHN gene in the mouse genome. Detailed methodologies for homologous recombination in mice are 5 available (see Capecchi, *Science* (1989) 244:1288-1292; Joyner *et al.*, *Nature* (1989) 338:153-156). Procedures for the production of non-rodent transgenic mammals and other animals are also available (Houdebine and Chourrout, *supra*; Pursel *et al.*, *Science* (1989) 244:1281-1288; Simms *et al.*, *Bio/Technology* (1988) 6:179-183). In a preferred embodiment, knock-out animals, such as mice harboring a knockout of a specific gene, 10 may be used to produce antibodies against the human counterpart of the gene that has been knocked out (Claesson MH *et al.*, (1994) *Scan J Immunol* 40:257-264; Declerck PJ *et al.*, (1995) *J Biol Chem*. 270:8397-400).

In another embodiment, the transgenic animal is a "knock-in" animal having an alteration in its genome that results in altered expression (e.g., increased (including 15 ectopic) or decreased expression) of the WHN gene, e.g., by introduction of additional copies of WHN, or by operatively inserting a regulatory sequence that provides for altered expression of an endogenous copy of the WHN gene. Such regulatory sequences include inducible, tissue-specific, and constitutive promoters and enhancer elements. The knock-in can be homozygous or heterozygous.

20 Transgenic nonhuman animals can also be produced that contain selected systems allowing for regulated expression of the transgene. One example of such a system that may be produced is the cre/loxP recombinase system of bacteriophage P1 (Lakso *et al.*, *PNAS* (1992) 89:6232-6236; U.S. Pat. No. 4,959,317). If a cre/loxP recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding 25 both the Cre recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, e.g., by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman *et al.* 30 (1991) *Science* 251:1351-1355; U.S. Pat. No. 5,654,182). In a preferred embodiment, both Cre-LoxP and Flp-Frt are used in the same system to regulate expression of the transgene, and for sequential deletion of vector sequences in the same cell (Sun X *et al* (2000) *Nat Genet* 25:83-6).

The genetically modified animals can be used in genetic studies to further elucidate the p21, p53, or branching morphogenesis pathway, as animal models of disease and disorders implicating defective p21, p53, or branching morphogenesis function, and for *in vivo* testing of candidate therapeutic agents, such as those identified in screens described below. The candidate therapeutic agents are administered to a genetically modified animal having altered WHN function and phenotypic changes are compared with appropriate control animals such as genetically modified animals that receive placebo treatment, and/or animals with unaltered WHN expression that receive candidate therapeutic agent.

In addition to the above-described genetically modified animals having altered WHN function, animal models having defective p21, p53, or branching morphogenesis function (and otherwise normal WHN function), can be used in the methods of the present invention. For example, a p21 or p53 knockout mouse can be used to assess, *in vivo*, the activity of a candidate p21, p53, or branching morphogenesis modulating agent identified in one of the *in vitro* assays described below. p21 and p53 knockout mice are described in the literature (Jacks et al., Nature 2001;410:1111-1116, 1043-1044; Donehower et al., supra; Umanoff H, et al., Proc Natl Acad Sci U S A 1995 Feb 28;92(5):1709-13). Preferably, the candidate p21, p53, or branching morphogenesis modulating agent when administered to a model system with cells defective in p21, p53, or branching morphogenesis function, produces a detectable phenotypic change in the model system indicating that the p21, p53, or branching morphogenesis function is restored, e.g., the cells exhibit normal cell cycle progression.

Modulating Agents

The invention provides methods to identify agents that interact with and/or modulate the function of WHN and/or the p21, p53, or branching morphogenesis pathway. Modulating agents identified by the methods are also part of the invention. Such agents are useful in a variety of diagnostic and therapeutic applications associated with the p21, p53, or branching morphogenesis pathway, as well as in further analysis of the WHN protein and its contribution to the p21, p53, or branching morphogenesis pathways. Accordingly, the invention also provides methods for modulating the p21, p53, or branching morphogenesis pathway comprising the step of specifically modulating WHN activity by administering a WHN-interacting or -modulating agent.

As used herein, a "WHN-modulating agent" is any agent that modulates WHN function, for example, an agent that interacts with WHN to inhibit or enhance WHN

activity or otherwise affect normal WHN function. WHN function can be affected at any level, including transcription, protein expression, protein localization, and cellular or extra-cellular activity. In a preferred embodiment, the WHN - modulating agent specifically modulates the function of the WHN. The phrases "specific modulating agent", "specifically modulates", etc., are used herein to refer to modulating agents that directly bind to the WHN polypeptide or nucleic acid, and preferably inhibit, enhance, or otherwise alter, the function of the WHN. These phrases also encompasses modulating agents that alter the interaction of the WHN with a binding partner, substrate, or cofactor (e.g. by binding to a binding partner of a WHN, or to a protein/binding partner complex, and altering WHN function). In a further preferred embodiment, the WHN- modulating agent is a modulator of the p21, p53, or branching morphogenesis pathway (e.g. it restores and/or upregulates p21, p53, or branching morphogenesis function) and thus is also a p21, p53, or branching morphogenesis-modulating agent.

Preferred WHN-modulating agents include small molecule compounds; WHN-interacting proteins, including antibodies and other biotherapeutics; and nucleic acid modulators such as antisense and RNA inhibitors. The modulating agents may be formulated in pharmaceutical compositions, for example, as compositions that may comprise other active ingredients, as in combination therapy, and/or suitable carriers or excipients. Techniques for formulation and administration of the compounds may be found in "Remington's Pharmaceutical Sciences" Mack Publishing Co., Easton, PA, 19th edition.

Small molecule modulators

Small molecules are often preferred to modulate function of proteins with enzymatic function, and/or containing protein interaction domains. Chemical agents, referred to in the art as "small molecule" compounds are typically organic, non-peptide molecules, having a molecular weight less than 10,000, preferably less than 5,000, more preferably less than 1,000, and most preferably less than 500. This class of modulators includes chemically synthesized molecules, for instance, compounds from combinatorial chemical libraries. Synthetic compounds may be rationally designed or identified based on known or inferred properties of the WHN protein or may be identified by screening compound libraries. Alternative appropriate modulators of this class are natural products, particularly secondary metabolites from organisms such as plants or fungi, which can also be identified by screening compound libraries for WHN-modulating activity. Methods for

generating and obtaining compounds are well known in the art (Schreiber SL, Science (2000) 151: 1964-1969; Radmann J and Gunther J, Science (2000) 151:1947-1948).

Small molecule modulators identified from screening assays, as described below, can be used as lead compounds from which candidate clinical compounds may be
5 designed, optimized, and synthesized. Such clinical compounds may have utility in treating pathologies associated with the p21, p53, or branching morphogenesis pathway. The activity of candidate small molecule modulating agents may be improved several-fold through iterative secondary functional validation, as further described below, structure determination, and candidate modulator modification and testing. Additionally, candidate
10 clinical compounds are generated with specific regard to clinical and pharmacological properties. For example, the reagents may be derivatized and re-screened using *in vitro* and *in vivo* assays to optimize activity and minimize toxicity for pharmaceutical development.

15 **Protein Modulators**

Specific WHN-interacting proteins are useful in a variety of diagnostic and therapeutic applications related to the p21, p53, or branching morphogenesis pathway and related disorders, as well as in validation assays for other WHN-modulating agents. In a preferred embodiment, WHN-interacting proteins affect normal WHN function, including
20 transcription, protein expression, protein localization, and cellular or extra-cellular activity. In another embodiment, WHN-interacting proteins are useful in detecting and providing information about the function of WHN proteins, as is relevant to p21, p53, or branching morphogenesis related disorders, such as cancer (e.g., for diagnostic means).

A WHN-interacting protein may be endogenous, i.e. one that naturally interacts
25 genetically or biochemically with a WHN, such as a member of the WHN pathway that modulates WHN expression, localization, and/or activity. WHN-modulators include dominant negative forms of WHN-interacting proteins and of WHN proteins themselves. Yeast two-hybrid and variant screens offer preferred methods for identifying endogenous WHN-interacting proteins (Finley, R. L. et al. (1996) in DNA Cloning-Expression
30 Systems: A Practical Approach, eds. Glover D. & Hames B. D (Oxford University Press, Oxford, England), pp. 169-203; Fashema SF et al., Gene (2000) 250:1-14; Drees BL Curr Opin Chem Biol (1999) 3:64-70; Vidal M and Legrain P Nucleic Acids Res (1999) 27:919-29; and U.S. Pat. No. 5,928,868). Mass spectrometry is an alternative preferred

method for the elucidation of protein complexes (reviewed in, e.g., Pandley A and Mann M, *Nature* (2000) 405:837-846; Yates JR 3rd, *Trends Genet* (2000) 16:5-8).

An WHN-interacting protein may be an exogenous protein, such as a WHN-specific antibody or a T-cell antigen receptor (see, e.g., Harlow and Lane (1988)

- 5 Antibodies, A Laboratory Manual, Cold Spring Harbor Laboratory; Harlow and Lane (1999) *Using antibodies: a laboratory manual*. Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press). WHN antibodies are further discussed below.

In preferred embodiments, a WHN-interacting protein specifically binds a WHN protein. In alternative preferred embodiments, a WHN-modulating agent binds a WHN substrate, binding partner, or cofactor.

Antibodies

In another embodiment, the protein modulator is a WHN specific antibody agonist or antagonist. The antibodies have therapeutic and diagnostic utilities, and can be used in screening assays to identify WHN modulators. The antibodies can also be used in dissecting the portions of the WHN pathway responsible for various cellular responses and in the general processing and maturation of the WHN.

Antibodies that specifically bind WHN polypeptides can be generated using known methods. Preferably the antibody is specific to a mammalian ortholog of WHN polypeptide, and more preferably, to human WHN. Antibodies may be polyclonal, monoclonal (mAbs), humanized or chimeric antibodies, single chain antibodies, Fab fragments, F(ab').sub.2 fragments, fragments produced by a FAb expression library, anti-idiotypic (anti-Id) antibodies, and epitope-binding fragments of any of the above. Epitopes of WHN which are particularly antigenic can be selected, for example, by routine screening of WHN polypeptides for antigenicity or by applying a theoretical method for selecting antigenic regions of a protein (Hopp and Wood (1981), *Proc. Nati. Acad. Sci. U.S.A.* 78:3824-28; Hopp and Wood, (1983) *Mol. Immunol.* 20:483-89; Sutcliffe et al., (1983) *Science* 219:660-66) to the amino acid sequence of a WHN. Monoclonal antibodies with affinities of 10^8 M^{-1} preferably 10^9 M^{-1} to 10^{10} M^{-1} , or stronger can be made by standard procedures as described (Harlow and Lane, *supra*; Goding (1986) *Monoclonal Antibodies: Principles and Practice* (2d ed) Academic Press, New York; and U.S. Pat. Nos. 4,381,292; 4,451,570; and 4,618,577). Antibodies may be generated against crude cell extracts of WHN or substantially purified fragments thereof. If WHN fragments are used, they preferably comprise at least 10, and more preferably, at least 20

contiguous amino acids of a WHN protein. In a particular embodiment, WHN-specific antigens and/or immunogens are coupled to carrier proteins that stimulate the immune response. For example, the subject polypeptides are covalently coupled to the keyhole limpet hemocyanin (KLH) carrier, and the conjugate is emulsified in Freund's complete adjuvant, which enhances the immune response. An appropriate immune system such as a laboratory rabbit or mouse is immunized according to conventional protocols.

The presence of WHN-specific antibodies is assayed by an appropriate assay such as a solid phase enzyme-linked immunosorbant assay (ELISA) using immobilized corresponding WHN polypeptides. Other assays, such as radioimmunoassays or fluorescent assays might also be used.

Chimeric antibodies specific to WHN polypeptides can be made that contain different portions from different animal species. For instance, a human immunoglobulin constant region may be linked to a variable region of a murine mAb, such that the antibody derives its biological activity from the human antibody, and its binding specificity from the murine fragment. Chimeric antibodies are produced by splicing together genes that encode the appropriate regions from each species (Morrison et al., Proc. Natl. Acad. Sci. (1984) 81:6851-6855; Neuberger et al., Nature (1984) 312:604-608; Takeda et al., Nature (1985) 31:452-454). Humanized antibodies, which are a form of chimeric antibodies, can be generated by grafting complementary-determining regions (CDRs) (Carlos, T. M., J. M. Harlan. 1994. Blood 84:2068-2101) of mouse antibodies into a background of human framework regions and constant regions by recombinant DNA technology (Riechmann LM, et al., 1988 Nature 323: 323-327). Humanized antibodies contain ~10% murine sequences and ~90% human sequences, and thus further reduce or eliminate immunogenicity, while retaining the antibody specificities (Co MS, and Queen C. 1991 Nature 351: 501-501; Morrison SL. 1992 Ann. Rev. Immun. 10:239-265). Humanized antibodies and methods of their production are well-known in the art (U.S. Pat. Nos. 5,530,101, 5,585,089, 5,693,762, and 6,180,370).

WHN-specific single chain antibodies which are recombinant, single chain polypeptides formed by linking the heavy and light chain fragments of the Fv regions via an amino acid bridge, can be produced by methods known in the art (U.S. Pat. No. 4,946,778; Bird, Science (1988) 242:423-426; Huston et al., Proc. Natl. Acad. Sci. USA (1988) 85:5879-5883; and Ward et al., Nature (1989) 334:544-546).

Other suitable techniques for antibody production involve in vitro exposure of lymphocytes to the antigenic polypeptides or alternatively to selection of libraries of

antibodies in phage or similar vectors (Huse et al., *Science* (1989) 246:1275-1281). As used herein, T-cell antigen receptors are included within the scope of antibody modulators (Harlow and Lane, 1988, *supra*).

The polypeptides and antibodies of the present invention may be used with or without modification. Frequently, antibodies will be labeled by joining, either covalently or non-covalently, a substance that provides for a detectable signal, or that is toxic to cells that express the targeted protein (Menard S, et al., *Int J. Biol Markers* (1989) 4:131-134). A wide variety of labels and conjugation techniques are known and are reported extensively in both the scientific and patent literature. Suitable labels include radionuclides, enzymes, substrates, cofactors, inhibitors, fluorescent moieties, fluorescent emitting lanthanide metals, chemiluminescent moieties, bioluminescent moieties, magnetic particles, and the like (U.S. Pat. Nos. 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149; and 4,366,241). Also, recombinant immunoglobulins may be produced (U.S. Pat. No. 4,816,567). Antibodies to cytoplasmic polypeptides may be delivered and reach their targets by conjugation with membrane-penetrating toxin proteins (U.S. Pat. No. 6,086,900).

When used therapeutically in a patient, the antibodies of the subject invention are typically administered parenterally, when possible at the target site, or intravenously. The therapeutically effective dose and dosage regimen is determined by clinical studies.

Typically, the amount of antibody administered is in the range of about 0.1 mg/kg –to about 10 mg/kg of patient weight. For parenteral administration, the antibodies are formulated in a unit dosage injectable form (e.g., solution, suspension, emulsion) in association with a pharmaceutically acceptable vehicle. Such vehicles are inherently nontoxic and non-therapeutic. Examples are water, saline, Ringer's solution, dextrose solution, and 5% human serum albumin. Nonaqueous vehicles such as fixed oils, ethyl oleate, or liposome carriers may also be used. The vehicle may contain minor amounts of additives, such as buffers and preservatives, which enhance isotonicity and chemical stability or otherwise enhance therapeutic potential. The antibodies' concentrations in such vehicles are typically in the range of about 1 mg/ml to about 10 mg/ml.

Immunotherapeutic methods are further described in the literature (US Pat. No. 5,859,206; WO0073469).

Nucleic Acid Modulators

Other preferred WHN-modulating agents comprise nucleic acid molecules, such as antisense oligomers or double stranded RNA (dsRNA), which generally inhibit WHN activity. Preferred nucleic acid modulators interfere with the function of the WHN nucleic acid such as DNA replication, transcription, translocation of the WHN RNA to the site of protein translation, translation of protein from the WHN RNA, splicing of the WHN RNA to yield one or more mRNA species, or catalytic activity which may be engaged in or facilitated by the WHN RNA.

In one embodiment, the antisense oligomer is an oligonucleotide that is sufficiently complementary to a WHN mRNA to bind to and prevent translation, preferably by binding to the 5' untranslated region. WHN-specific antisense oligonucleotides, preferably range from at least 6 to about 200 nucleotides. In some embodiments the oligonucleotide is preferably at least 10, 15, or 20 nucleotides in length. In other embodiments, the oligonucleotide is preferably less than 50, 40, or 30 nucleotides in length. The 10 oligonucleotide can be DNA or RNA or a chimeric mixture or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone. The oligonucleotide may include other appending groups such as peptides, agents that facilitate transport across the cell membrane, hybridization-triggered cleavage agents, and intercalating agents.

15

In another embodiment, the antisense oligomer is a phosphothioate morpholino oligomer (PMO). PMOs are assembled from four different morpholino subunits, each of which contain one of four genetic bases (A, C, G, or T) linked to a six-membered morpholine ring. Polymers of these subunits are joined by non-ionic phosphodiamidate intersubunit linkages. Details of how to make and use PMOs and other antisense 20 oligomers are well known in the art (e.g. see WO99/18193; Probst JC, Antisense Oligodeoxynucleotide and Ribozyme Design, Methods. (2000) 22(3):271-281; Summerton J, and Weller D. 1997 Antisense Nucleic Acid Drug Dev. :7:187-95; US Pat. No. 25 5,235,033; and US Pat No. 5,378,841).

Alternative preferred WHN nucleic acid modulators are double-stranded RNA 30 species mediating RNA interference (RNAi). RNAi is the process of sequence-specific, post-transcriptional gene silencing in animals and plants, initiated by double-stranded RNA (dsRNA) that is homologous in sequence to the silenced gene. Methods relating to the use of RNAi to silence genes in *C. elegans*, *Drosophila*, plants, and humans are known in the art (Fire A, et al., 1998 Nature 391:806-811; Fire, A. Trends Genet. 15, 358-363

(1999); Sharp, P. A. RNA interference 2001. *Genes Dev.* 15, 485-490 (2001); Hammond, S. M., et al., *Nature Rev. Genet.* 2, 110-1119 (2001); Tuschl, T. *Chem. Biochem.* 2, 239-245 (2001); Hamilton, A. et al., *Science* 286, 950-952 (1999); Hammond, S. M., et al., *Nature* 404, 293-296 (2000); Zamore, P. D., et al., *Cell* 101, 25-33 (2000); Bernstein, E., 5 et al., *Nature* 409, 363-366 (2001); Elbashir, S. M., et al., *Genes Dev.* 15, 188-200 (2001); WO0129058; WO9932619; Elbashir SM, et al., 2001 *Nature* 411:494-498).

Nucleic acid modulators are commonly used as research reagents, diagnostics, and therapeutics. For example, antisense oligonucleotides, which are able to inhibit gene expression with exquisite specificity, are often used to elucidate the function of particular 10 genes (see, for example, U.S. Pat. No. 6,165,790). Nucleic acid modulators are also used, for example, to distinguish between functions of various members of a biological pathway. For example, antisense oligomers have been employed as therapeutic moieties in the treatment of disease states in animals and man and have been demonstrated in numerous 15 clinical trials to be safe and effective (Milligan JF, *et al.*, *Current Concepts in Antisense Drug Design*, *J Med Chem.* (1993) 36:1923-1937; Tonkinson JL *et al.*, *Antisense Oligodeoxynucleotides as Clinical Therapeutic Agents*, *Cancer Invest.* (1996) 14:54-65). Accordingly, in one aspect of the invention, a WHN-specific nucleic acid modulator is used in an assay to further elucidate the role of the WHN in the p21, p53, or branching 20 morphogenesis pathway, and/or its relationship to other members of the pathway. In another aspect of the invention, a WHN-specific antisense oligomer is used as a therapeutic agent for treatment of p21, p53, or branching morphogenesis-related disease states.

Assay Systems

The invention provides assay systems and screening methods for identifying 25 specific modulators of WHN activity. As used herein, an "assay system" encompasses all the components required for performing and analyzing results of an assay that detects and/or measures a particular event. In general, primary assays are used to identify or confirm a modulator's specific biochemical or molecular effect with respect to the WHN 30 nucleic acid or protein. In general, secondary assays further assess the activity of a WHN modulating agent identified by a primary assay and may confirm that the modulating agent affects WHN in a manner relevant to the p21, p53, or branching morphogenesis pathway. In some cases, WHN modulators will be directly tested in a secondary assay.

In a preferred embodiment, the screening method comprises contacting a suitable assay system comprising a WHN polypeptide or nucleic acid with a candidate agent under conditions whereby, but for the presence of the agent, the system provides a reference activity (e.g. binding activity), which is based on the particular molecular event the screening method detects. A statistically significant difference between the agent-biased activity and the reference activity indicates that the candidate agent modulates WHN activity, and hence the p21, p53, or branching morphogenesis pathway. The WHN polypeptide or nucleic acid used in the assay may comprise any of the nucleic acids or polypeptides described above.

10

Primary Assays

The type of modulator tested generally determines the type of primary assay.

Primary assays for small molecule modulators

For small molecule modulators, screening assays are used to identify candidate modulators. Screening assays may be cell-based or may use a cell-free system that recreates or retains the relevant biochemical reaction of the target protein (reviewed in Sittampalam GS *et al.*, Curr Opin Chem Biol (1997) 1:384-91 and accompanying references). As used herein the term "cell-based" refers to assays using live cells, dead cells, or a particular cellular fraction, such as a membrane, endoplasmic reticulum, or mitochondrial fraction. The term "cell free" encompasses assays using substantially purified protein (either endogenous or recombinantly produced), partially purified or crude cellular extracts. Screening assays may detect a variety of molecular events, including protein-DNA interactions, protein-protein interactions (e.g., receptor-ligand binding), transcriptional activity (e.g., using a reporter gene), enzymatic activity (e.g., via a property of the substrate), activity of second messengers, immunogenicity and changes in cellular morphology or other cellular characteristics. Appropriate screening assays may use a wide range of detection methods including fluorescent, radioactive, colorimetric, spectrophotometric, and amperometric methods, to provide a read-out for the particular molecular event detected.

Cell-based screening assays usually require systems for recombinant expression of WHN and any auxiliary proteins demanded by the particular assay. Appropriate methods for generating recombinant proteins produce sufficient quantities of proteins that retain their relevant biological activities and are of sufficient purity to optimize activity and

assure assay reproducibility. Yeast two-hybrid and variant screens, and mass spectrometry provide preferred methods for determining protein-protein interactions and elucidation of protein complexes. In certain applications, when WHN-interacting proteins are used in screens to identify small molecule modulators, the binding specificity of the interacting 5 protein to the WHN protein may be assayed by various known methods such as substrate processing (e.g. ability of the candidate WHN-specific binding agents to function as negative effectors in WHN-expressing cells), binding equilibrium constants (usually at least about 10^7 M^{-1} , preferably at least about 10^8 M^{-1} , more preferably at least about 10^9 M^{-1}), and immunogenicity (e.g. ability to elicit WHN specific antibody in a heterologous host 10 such as a mouse, rat, goat or rabbit). For enzymes and receptors, binding may be assayed by, respectively, substrate and ligand processing.

The screening assay may measure a candidate agent's ability to specifically bind to or modulate activity of a WHN polypeptide, a fusion protein thereof, or to cells or membranes bearing the polypeptide or fusion protein. The WHN polypeptide can be full 15 length or a fragment thereof that retains functional WHN activity. The WHN polypeptide may be fused to another polypeptide, such as a peptide tag for detection or anchoring, or to another tag. The WHN polypeptide is preferably human WHN, or is an ortholog or derivative thereof as described above. In a preferred embodiment, the screening assay detects candidate agent-based modulation of WHN interaction with a binding target, such 20 as an endogenous or exogenous protein or other substrate that has WHN -specific binding activity, and can be used to assess normal WHN gene function.

Suitable assay formats that may be adapted to screen for WHN modulators are known in the art. Preferred screening assays are high throughput or ultra high throughput and thus provide automated, cost-effective means of screening compound libraries for lead 25 compounds (Fernandes PB, Curr Opin Chem Biol (1998) 2:597-603; Sundberg SA, Curr Opin Biotechnol 2000, 11:47-53). In one preferred embodiment, screening assays uses fluorescence technologies, including fluorescence polarization, time-resolved 30 fluorescence, and fluorescence resonance energy transfer. These systems offer means to monitor protein-protein or DNA-protein interactions in which the intensity of the signal emitted from dye-labeled molecules depends upon their interactions with partner molecules (e.g., Selvin PR, Nat Struct Biol (2000) 7:730-4; Fernandes PB, *supra*; Hertzberg RP and Pope AJ, Curr Opin Chem Biol (2000) 4:445-451).

A variety of suitable assay systems may be used to identify candidate WHN and p21, p53, or branching morphogenesis pathway modulators (e.g. U.S. Pat. Nos. 5,550,019

and 6,133,437 (apoptosis assays); U.S. Pat. No. 6,020,135 (p53 modulation), U.S. Pat. Nos. 5,976,782, 6,225,118 and 6,444,434 (angiogenesis assays), among others). Specific preferred assays are described in more detail below.

Transcription factors control gene transcription. Electrophoretic mobility shift assay (EMSA) or gel shift assay is one of the most powerful methods for studying protein-DNA interactions. High throughput gel shift assays for transcription factors may involve fluorescence (Cyano dye Cy5) labeled oligodeoxynucleotide duplexes as specific probes and an automatic DNA sequencer for analysis (Ruscher K, et al., (2000) J Biotechnol 78:163-70). Alternatively high throughput methods involve colorimetric assays (Renard P, et al. (2001) Nucleic Acids Res 29(4):E21), or homogeneous fluorescence assays for the detection and quantification of sequence-specific DNA-binding proteins (Heyduk T, and Heyduk E (2001) Nat Biotechnol 20:171-6.)

Apoptosis assays. Assays for apoptosis may be performed by terminal deoxynucleotidyl transferase-mediated digoxigenin-11-dUTP nick end labeling (TUNEL) assay. The TUNEL assay is used to measure nuclear DNA fragmentation characteristic of apoptosis (Lazebnik *et al.*, 1994, Nature 371, 346), by following the incorporation of fluorescein-dUTP (Yonehara *et al.*, 1989, J. Exp. Med. 169, 1747). Apoptosis may further be assayed by acridine orange staining of tissue culture cells (Lucas, R., et al., 1998, Blood 15:4730-41). An apoptosis assay system may comprise a cell that expresses a WHN, and that optionally has defective p21, p53, or branching morphogenesis function (e.g. p21, p53 is over-expressed or under-expressed, or branching morphogenesis is increased or decreased, relative to wild-type cells). A test agent can be added to the apoptosis assay system and changes in induction of apoptosis relative to controls where no test agent is added, identify candidate p21, p53, or branching morphogenesis modulating agents. In some embodiments of the invention, an apoptosis assay may be used as a secondary assay to test a candidate p21, p53, or branching morphogenesis modulating agents that is initially identified using a cell-free assay system. An apoptosis assay may also be used to test whether WHN function plays a direct role in apoptosis. For example, an apoptosis assay may be performed on cells that over- or under-express WHN relative to wild type cells. Differences in apoptotic response compared to wild type cells suggests that the WHN plays a direct role in the apoptotic response. Apoptosis assays are described further in US Pat. No. 6,133,437.

Cell proliferation and cell cycle assays. Cell proliferation may be assayed via bromodeoxyuridine (BRDU) incorporation. This assay identifies a cell population undergoing DNA synthesis by incorporation of BRDU into newly-synthesized DNA. Newly-synthesized DNA may then be detected using an anti-BRDU antibody (Hoshino *et al.*, 1986, Int. J. Cancer 38, 369; Campana *et al.*, 1988, J. Immunol. Meth. 107, 79), or by other means.

Cell Proliferation may also be examined using [³H]-thymidine incorporation (Chen, J., 1996, Oncogene 13:1395-403; Jeoung, J., 1995, J. Biol. Chem. 270:18367-73). This assay allows for quantitative characterization of S-phase DNA syntheses. In this assay, cells synthesizing DNA will incorporate [³H]-thymidine into newly synthesized DNA. Incorporation can then be measured by standard techniques such as by counting of radioisotope in a scintillation counter (e.g., Beckman LS 3800 Liquid Scintillation Counter). Another proliferation assay uses the dye Alamar Blue (available from Biosource International), which fluoresces when reduced in living cells and provides an indirect measurement of cell number (Voystik-Harbin SL *et al.*, 1998, In Vitro Cell Dev Biol Anim 34:239-46).

Cell proliferation may also be assayed by colony formation in soft agar (Sambrook *et al.*, Molecular Cloning, Cold Spring Harbor (1989)). For example, cells transformed with WHN are seeded in soft agar plates, and colonies are measured and counted after two weeks incubation.

Involvement of a gene in the cell cycle may be assayed by flow cytometry (Gray JW *et al.* (1986) Int J Radiat Biol Relat Stud Phys Chem Med 49:237-55). Cells transfected with a WHN may be stained with propidium iodide and evaluated in a flow cytometer (available from Becton Dickinson), which indicates accumulation of cells in different stages of the cell cycle.

Accordingly, a cell proliferation or cell cycle assay system may comprise a cell that expresses a WHN, and that optionally has defective p21, p53, or branching morphogenesis function (e.g. p21, p53 is over-expressed or under-expressed, or branching morphogenesis is increased or decreased, relative to wild-type cells). A test agent can be added to the assay system and changes in cell proliferation or cell cycle relative to controls where no test agent is added, identify candidate p21, p53, or branching morphogenesis modulating agents. In some embodiments of the invention, the cell proliferation or cell cycle assay may be used as a secondary assay to test a candidate p21, p53, or branching morphogenesis modulating agents that is initially identified using another assay system

such as a cell-free assay system. A cell proliferation assay may also be used to test whether WHN function plays a direct role in cell proliferation or cell cycle. For example, a cell proliferation or cell cycle assay may be performed on cells that over- or under-express WHN relative to wild type cells. Differences in proliferation or cell cycle 5 compared to wild type cells suggests that the WHN plays a direct role in cell proliferation or cell cycle.

Angiogenesis. Angiogenesis may be assayed using various human endothelial cell systems, such as umbilical vein, coronary artery, or dermal cells. Suitable assays include 10 Alamar Blue based assays (available from Biosource International) to measure proliferation; migration assays using fluorescent molecules, such as the use of Becton Dickinson Falcon HTS FluoroBlock cell culture inserts to measure migration of cells through membranes in presence or absence of angiogenesis enhancer or suppressors; and tubule formation assays based on the formation of tubular structures by endothelial cells 15 on Matrigel® (Becton Dickinson). Accordingly, an angiogenesis assay system may comprise a cell that expresses a WHN, and that optionally has defective p21, p53, or branching morphogenesis function (e.g. p21, p53 is over-expressed or under-expressed, or branching morphogenesis is increased or decreased, relative to wild-type cells). A test agent can be added to the angiogenesis assay system and changes in angiogenesis relative 20 to controls where no test agent is added, identify candidate p21, p53, or branching morphogenesis modulating agents. In some embodiments of the invention, the angiogenesis assay may be used as a secondary assay to test a candidate p21, p53, or branching morphogenesis modulating agents that is initially identified using another assay system. An angiogenesis assay may also be used to test whether WHN function plays a 25 direct role in cell proliferation. For example, an angiogenesis assay may be performed on cells that over- or under-express WHN relative to wild type cells. Differences in angiogenesis compared to wild type cells suggests that the WHN plays a direct role in angiogenesis. U.S. Pat. Nos. 5,976,782, 6,225,118 and 6,444,434, among others.

30 **Hypoxic induction.** The alpha subunit of the transcription factor, hypoxia inducible factor-1 (HIF-1), is upregulated in tumor cells following exposure to hypoxia in vitro. Under hypoxic conditions, HIF-1 stimulates the expression of genes known to be important in tumour cell survival, such as those encoding glyolytic enzymes and VEGF. Induction of such genes by hypoxic conditions may be assayed by growing cells

transfected with WHN in hypoxic conditions (such as with 0.1% O₂, 5% CO₂, and balance N₂, generated in a Napco 7001 incubator (Precision Scientific)) and normoxic conditions, followed by assessment of gene activity or expression by Taqman®. For example, a hypoxic induction assay system may comprise a cell that expresses a WHN, 5 and that optionally has a mutated p21, p53, or branching morphogenesis (e.g. p21, p53 is over-expressed or under-expressed, or branching morphogenesis is increased or decreased, relative to wild-type cells). A test agent can be added to the hypoxic induction assay system and changes in hypoxic response relative to controls where no test agent is added, identify candidate p21, p53, or branching morphogenesis modulating agents. In some 10 embodiments of the invention, the hypoxic induction assay may be used as a secondary assay to test a candidate p21, p53, or branching morphogenesis modulating agents that is initially identified using another assay system. A hypoxic induction assay may also be used to test whether WHN function plays a direct role in the hypoxic response. For example, a hypoxic induction assay may be performed on cells that over- or under-express 15 WHN relative to wild type cells. Differences in hypoxic response compared to wild type cells suggests that the WHN plays a direct role in hypoxic induction.

Cell adhesion. Cell adhesion assays measure adhesion of cells to purified adhesion proteins, or adhesion of cells to each other, in presence or absence of candidate 20 modulating agents. Cell-protein adhesion assays measure the ability of agents to modulate the adhesion of cells to purified proteins. For example, recombinant proteins are produced, diluted to 2.5g/mL in PBS, and used to coat the wells of a microtiter plate. The wells used for negative control are not coated. Coated wells are then washed, blocked with 1% BSA, and washed again. Compounds are diluted to 2× final test concentration 25 and added to the blocked, coated wells. Cells are then added to the wells, and the unbound cells are washed off. Retained cells are labeled directly on the plate by adding a membrane-permeable fluorescent dye, such as calcein-AM, and the signal is quantified in a fluorescent microplate reader.

Cell-cell adhesion assays measure the ability of agents to modulate binding of cell 30 adhesion proteins with their native ligands. These assays use cells that naturally or recombinantly express the adhesion protein of choice. In an exemplary assay, cells expressing the cell adhesion protein are plated in wells of a multiwell plate. Cells expressing the ligand are labeled with a membrane-permeable fluorescent dye, such as BCECF, and allowed to adhere to the monolayers in the presence of candidate agents.

Unbound cells are washed off, and bound cells are detected using a fluorescence plate reader.

High-throughput cell adhesion assays have also been described. In one such assay, small molecule ligands and peptides are bound to the surface of microscope slides using a 5 microarray spotter, intact cells are then contacted with the slides, and unbound cells are washed off. In this assay, not only the binding specificity of the peptides and modulators against cell lines are determined, but also the functional cell signaling of attached cells using immunofluorescence techniques *in situ* on the microchip is measured (Falsey JR et al., Bioconjug Chem. 2001 May-Jun;12(3):346-53).

10

Tubulogenesis. Tubulogenesis assays monitor the ability of cultured cells, generally endothelial cells, to form tubular structures on a matrix substrate, which generally simulates the environment of the extracellular matrix. Exemplary substrates include Matrigel™ (Becton Dickinson), an extract of basement membrane proteins 15 containing laminin, collagen IV, and heparin sulfate proteoglycan, which is liquid at 4°C and forms a solid gel at 37°C. Other suitable matrices comprise extracellular components such as collagen, fibronectin, and/or fibrin. Cells are stimulated with a pro-angiogenic stimulant, and their ability to form tubules is detected by imaging. Tubules can generally be detected after an overnight incubation with stimuli, but longer or shorter time frames 20 may also be used. Tube formation assays are well known in the art (e.g., Jones MK et al., 1999, Nature Medicine 5:1418-1423). These assays have traditionally involved stimulation with serum or with the growth factors FGF or VEGF. Serum represents an undefined source of growth factors. In a preferred embodiment, the assay is performed 25 with cells cultured in serum free medium, in order to control which process or pathway a candidate agent modulates. Moreover, we have found that different target genes respond differently to stimulation with different pro-angiogenic agents, including inflammatory angiogenic factors such as TNF-alpha. Thus, in a further preferred embodiment, a tubulogenesis assay system comprises testing a WHN's response to a variety of factors, such as FGF, VEGF, phorbol myristate acetate (PMA), TNF-alpha, ephrin, etc.

30

Cell Migration. An invasion/migration assay (also called a migration assay) tests the ability of cells to overcome a physical barrier and to migrate towards pro-angiogenic signals. Migration assays are known in the art (e.g., Paik JH et al., 2001, J Biol Chem 276:11830-11837). In a typical experimental set-up, cultured endothelial cells are seeded

onto a matrix-coated porous lamina, with pore sizes generally smaller than typical cell size. The matrix generally simulates the environment of the extracellular matrix, as described above. The lamina is typically a membrane, such as the transwell polycarbonate membrane (Corning Costar Corporation, Cambridge, MA), and is generally part of an upper chamber that is in fluid contact with a lower chamber containing pro-angiogenic stimuli. Migration is generally assayed after an overnight incubation with stimuli, but longer or shorter time frames may also be used. Migration is assessed as the number of cells that crossed the lamina, and may be detected by staining cells with hemotoxylin solution (VWR Scientific, South San Francisco, CA), or by any other method for determining cell number. In another exemplary set up, cells are fluorescently labeled and migration is detected using fluorescent readings, for instance using the Falcon HTS FluoroBlok (Becton Dickinson). While some migration is observed in the absence of stimulus, migration is greatly increased in response to pro-angiogenic factors. As described above, a preferred assay system for migration/invasion assays comprises testing a WHN's response to a variety of pro-angiogenic factors, including tumor angiogenic and inflammatory angiogenic agents, and culturing the cells in serum free medium.

Sprouting assay. A sprouting assay is a three-dimensional *in vitro* angiogenesis assay that uses a cell-number defined spheroid aggregation of endothelial cells ("spheroid"), embedded in a collagen gel-based matrix. The spheroid can serve as a starting point for the sprouting of capillary-like structures by invasion into the extracellular matrix (termed "cell sprouting") and the subsequent formation of complex anastomosing networks (Korff and Augustin, 1999, J Cell Sci 112:3249-58). In an exemplary experimental set-up, spheroids are prepared by pipetting 400 human umbilical vein endothelial cells into individual wells of a nonadhesive 96-well plates to allow overnight spheroidal aggregation (Korff and Augustin: J Cell Biol 143: 1341-52, 1998). Spheroids are harvested and seeded in 900 μ l of methocel-collagen solution and pipetted into individual wells of a 24 well plate to allow collagen gel polymerization. Test agents are added after 30 min by pipetting 100 μ l of 10-fold concentrated working dilution of the test substances on top of the gel. Plates are incubated at 37°C for 24h. Dishes are fixed at the end of the experimental incubation period by addition of paraformaldehyde. Sprouting intensity of endothelial cells can be quantitated by an automated image analysis system to determine the cumulative sprout length per spheroid.

Primary assays for antibody modulators

For antibody modulators, appropriate primary assays test is a binding assay that tests the antibody's affinity to and specificity for the WHN protein. Methods for testing antibody affinity and specificity are well known in the art (Harlow and Lane, 1988, 1999, 5 *supra*). The enzyme-linked immunosorbant assay (ELISA) is a preferred method for detecting WHN-specific antibodies; others include FACS assays, radioimmunoassays, and fluorescent assays.

In some cases, screening assays described for small molecule modulators may also be used to test antibody modulators.

10

Primary assays for nucleic acid modulators

For nucleic acid modulators, primary assays may test the ability of the nucleic acid modulator to inhibit or enhance WHN gene expression, preferably mRNA expression. In general, expression analysis comprises comparing WHN expression in like populations of 15 cells (*e.g.*, two pools of cells that endogenously or recombinantly express WHN) in the presence and absence of the nucleic acid modulator. Methods for analyzing mRNA and protein expression are well known in the art. For instance, Northern blotting, slot blotting, ribonuclease protection, quantitative RT-PCR (*e.g.*, using the TaqMan®, PE Applied Biosystems), or microarray analysis may be used to confirm that WHN mRNA expression 20 is reduced in cells treated with the nucleic acid modulator (*e.g.*, Current Protocols in Molecular Biology (1994) Ausubel FM *et al.*, *eds.*, John Wiley & Sons, Inc., chapter 4; Freeman WM *et al.*, Biotechniques (1999) 26:112-125; Kallioniemi OP, Ann Med 2001, 33:142-147; Blohm DH and Guiseppi-Elie, A Curr Opin Biotechnol 2001, 12:41-47). Protein expression may also be monitored. Proteins are most commonly detected with 25 specific antibodies or antisera directed against either the WHN protein or specific peptides. A variety of means including Western blotting, ELISA, or in situ detection, are available (Harlow E and Lane D, 1988 and 1999, *supra*).

In some cases, screening assays described for small molecule modulators, particularly in assay systems that involve WHN mRNA expression, may also be used to 30 test nucleic acid modulators.

Secondary Assays

Secondary assays may be used to further assess the activity of WHN-modulating agent identified by any of the above methods to confirm that the modulating agent affects

WHN in a manner relevant to the p21, p53, or branching morphogenesis pathway. As used herein, WHN-modulating agents encompass candidate clinical compounds or other agents derived from previously identified modulating agent. Secondary assays can also be used to test the activity of a modulating agent on a particular genetic or biochemical 5 pathway or to test the specificity of the modulating agent's interaction with WHN.

Secondary assays generally compare like populations of cells or animals (e.g., two pools of cells or animals that endogenously or recombinantly express WHN) in the presence and absence of the candidate modulator. In general, such assays test whether treatment of cells or animals with a candidate WHN-modulating agent results in changes 10 in the p21, p53, or branching morphogenesis pathway in comparison to untreated (or mock- or placebo-treated) cells or animals. Certain assays use "sensitized genetic backgrounds", which, as used herein, describe cells or animals engineered for altered expression of genes in the p21, p53, or branching morphogenesis or interacting pathways.

15 ***Cell-based assays***

Cell based assays may use a variety of mammalian cell lines known to have defective p21, p53, or branching morphogenesis function (e.g. SAOS-2 osteoblasts, H1299 lung cancer cells, C33A and HT3 cervical cancer cells, HT-29 and DLD-1 colon cancer cells, HCT116 colon cancer cells, among others, available from American Type Culture 20 Collection (ATCC), Manassas, VA). Cell based assays may detect endogenous p21, p53, or branching morphogenesis pathway activity or may rely on recombinant expression of p21, p53, or branching morphogenesis pathway components. Any of the aforementioned assays may be used in this cell-based format. Candidate modulators are typically added to the cell media but may also be injected into cells or delivered by any other efficacious 25 means.

Animal Assays

A variety of non-human animal models of normal or defective p21, p53, or branching morphogenesis pathway may be used to test candidate WHN modulators. 30 Models for defective p21, p53, or branching morphogenesis pathway typically use genetically modified animals that have been engineered to mis-express (e.g., over-express or lack expression in) genes involved in the p21, p53, or branching morphogenesis pathway. Assays generally require systemic delivery of the candidate modulators, such as by oral administration, injection, etc.

In a preferred embodiment, p21, p53, or branching morphogenesis pathway activity is assessed by monitoring neovascularization and angiogenesis. Animal models with defective and normal p21, p53, or branching morphogenesis are used to test the candidate modulator's affect on WHN in Matrigel® assays. Matrigel® is an extract of 5 basement membrane proteins, and is composed primarily of laminin, collagen IV, and heparin sulfate proteoglycan. It is provided as a sterile liquid at 4°C, but rapidly forms a solid gel at 37°C. Liquid Matrigel® is mixed with various angiogenic agents, such as bFGF and VEGF, or with human tumor cells which over-express the WHN. The mixture is then injected subcutaneously(SC) into female athymic nude mice (Taconic, 10 Germantown, NY) to support an intense vascular response. Mice with Matrigel® pellets may be dosed via oral (PO), intraperitoneal (IP), or intravenous (IV) routes with the candidate modulator. Mice are euthanized 5 - 12 days post-injection, and the Matrigel® pellet is harvested for hemoglobin analysis (Sigma plasma hemoglobin kit). Hemoglobin content of the gel is found to correlate the degree of neovascularization in the gel.

15 In another preferred embodiment, the effect of the candidate modulator on WHN is assessed via tumorigenicity assays. In one example, a xenograft comprising human cells from a pre-existing tumor or a tumor cell line known to be angiogenic is used; exemplary cell lines include A431, Colo205, MDA-MB-435, A673, A375, Calu-6, MDA-MB-231, 460, SF763T, or SKOV3tp5. Tumor xenograft assays are known in the art (see, e.g., 20 Ogawa K et al., 2000, Oncogene 19:6043-6052). Xenografts are typically implanted SC into female athymic mice, 6-7 week old, as single cell suspensions either from a pre-existing tumor or from *in vitro* culture. The tumors which express the WHN endogenously are injected in the flank, 1×10^5 to 1×10^7 cells per mouse in a volume of 25 100 μL using a 27gauge needle. Mice are then ear tagged and tumors are measured twice weekly. Candidate modulator treatment is initiated on the day the mean tumor weight reaches 100 mg. Candidate modulator is delivered IV, SC, IP, or PO by bolus administration. Depending upon the pharmacokinetics of each unique candidate modulator, dosing can be performed multiple times per day. The tumor weight is assessed by measuring perpendicular diameters with a caliper and calculated by multiplying the 30 measurements of diameters in two dimensions. At the end of the experiment, the excised tumors maybe utilized for biomarker identification or further analyses. For immunohistochemistry staining, xenograft tumors are fixed in 4% paraformaldehyde, 0.1M phosphate, pH 7.2, for 6 hours at 4°C, immersed in 30% sucrose in PBS, and rapidly frozen in isopentane cooled with liquid nitrogen.

In another preferred embodiment, tumorogenicity is monitored using a hollow fiber assay, which is described in U.S. Pat No. US 5,698,413. Briefly, the method comprises implanting into a laboratory animal a biocompatible, semi-permeable encapsulation device containing target cells, treating the laboratory animal with a candidate modulating agent, 5 and evaluating the target cells for reaction to the candidate modulator. Implanted cells are generally human cells from a pre-existing tumor or a tumor cell line known to be angiogenic. After an appropriate period of time, generally around six days, the implanted samples are harvested for evaluation of the candidate modulator. Tumorogenicity and modulator efficacy may be evaluated by assaying the quantity of viable cells present in the 10 macrocapsule, which can be determined by tests known in the art, for example, MTT dye conversion assay, neutral red dye uptake, trypan blue staining, viable cell counts, the number of colonies formed in soft agar, the capacity of the cells to recover and replicate in vitro, etc. Other assays specific to angiogenesis, as are known in the art and described herein, may also be used.

15 In another preferred embodiment, a tumorogenicity assay use a transgenic animal, usually a mouse, carrying a dominant oncogene or tumor suppressor gene knockout under the control of tissue specific regulatory sequences; these assays are generally referred to as transgenic tumor assays. In a preferred application, tumor development in the transgenic model is well characterized or is controlled. In an exemplary model, the "RIP1-Tag2" 20 transgene, comprising the SV40 large T-antigen oncogene under control of the insulin gene regulatory regions is expressed in pancreatic beta cells and results in islet cell carcinomas (Hanahan D, 1985, Nature 315:115-122; Parangi S et al, 1996, Proc Natl Acad Sci USA 93: 2002-2007; Bergers G et al, 1999, Science 284:808-812). An "angiogenic switch," occurs at approximately five weeks, as normally quiescent capillaries in a subset 25 of hyperproliferative islets become angiogenic. The RIP1-TAG2 mice die by age 14 weeks. Candidate modulators may be administered at a variety of stages, including just prior to the angiogenic switch (e.g., for a model of tumor prevention), during the growth of small tumors (e.g., for a model of intervention), or during the growth of large and/or invasive tumors (e.g., for a model of regression). Tumorogenicity and modulator efficacy 30 can be evaluating life-span extension and/or tumor characteristics, including number of tumors, tumor size, tumor morphology, vessel density, apoptotic index, etc.

Diagnostic and therapeutic uses

Specific WHN-modulating agents are useful in a variety of diagnostic and therapeutic applications where disease or disease prognosis is related to defects in the p21, p53, or branching morphogenesis pathway, such as angiogenic, apoptotic, or cell proliferation disorders. Accordingly, the invention also provides methods for modulating the p21, p53, or branching morphogenesis pathway in a cell, preferably a cell pre-determined to have defective or impaired p21, p53, or branching morphogenesis function (e.g. due to overexpression, underexpression, or misexpression of p21, p53, or branching morphogenesis, or due to gene mutations), comprising the step of administering an agent to the cell that specifically modulates WHN activity. Preferably, the modulating agent produces a detectable phenotypic change in the cell indicating that the p21, p53, or branching morphogenesis function is restored. The phrase "function is restored", and equivalents, as used herein, means that the desired phenotype is achieved, or is brought closer to normal compared to untreated cells. For example, with restored p21, p53, or branching morphogenesis function, cell proliferation and/or progression through cell cycle may normalize, or be brought closer to normal relative to untreated cells. The invention also provides methods for treating disorders or disease associated with impaired p21, p53, or branching morphogenesis function by administering a therapeutically effective amount of a WHN -modulating agent that modulates the p21, p53, or branching morphogenesis pathway. The invention further provides methods for modulating WHN function in a cell, preferably a cell pre-determined to have defective or impaired WHN function, by administering a WHN -modulating agent. Additionally, the invention provides a method for treating disorders or disease associated with impaired WHN function by administering a therapeutically effective amount of a WHN -modulating agent.

The discovery that WHN is implicated in p21, p53, or branching morphogenesis pathway provides for a variety of methods that can be employed for the diagnostic and prognostic evaluation of diseases and disorders involving defects in the p21, p53, or branching morphogenesis pathway and for the identification of subjects having a predisposition to such diseases and disorders.

Various expression analysis methods can be used to diagnose whether WHN expression occurs in a particular sample, including Northern blotting, slot blotting, ribonuclease protection, quantitative RT-PCR, and microarray analysis. (e.g., Current Protocols in Molecular Biology (1994) Ausubel FM *et al.*, eds., John Wiley & Sons, Inc., chapter 4; Freeman WM *et al.*, Biotechniques (1999) 26:112-125; Kallioniemi OP, Ann

Med 2001, 33:142-147; Blohm and Guiseppi-Elie, Curr Opin Biotechnol 2001, 12:41-47).

Tissues having a disease or disorder implicating defective p21, p53, or branching morphogenesis signaling that express a WHN, are identified as amenable to treatment with a WHN modulating agent. In a preferred application, the p21, p53, or branching

5 morphogenesis defective tissue overexpresses a WHN relative to normal tissue. For example, a Northern blot analysis of mRNA from tumor and normal cell lines, or from tumor and matching normal tissue samples from the same patient, using full or partial WHN cDNA sequences as probes, can determine whether particular tumors express or overexpress WHN. Alternatively, the TaqMan® is used for quantitative RT-PCR analysis
10 of WHN expression in cell lines, normal tissues and tumor samples (PE Applied Biosystems).

Various other diagnostic methods may be performed, for example, utilizing reagents such as the WHN oligonucleotides, and antibodies directed against a WHN, as described above for: (1) the detection of the presence of WHN gene mutations, or the
15 detection of either over- or under-expression of WHN mRNA relative to the non-disorder state; (2) the detection of either an over- or an under-abundance of WHN gene product relative to the non-disorder state; and (3) the detection of perturbations or abnormalities in the signal transduction pathway mediated by WHN.

Thus, in a specific embodiment, the invention is drawn to a method for diagnosing
20 a disease or disorder in a patient that is associated with alterations in WHN expression, the method comprising: a) obtaining a biological sample from the patient; b) contacting the sample with a probe for WHN expression; c) comparing results from step (b) with a control; and d) determining whether step (c) indicates a likelihood of the disease or disorder. Preferably, the disease is cancer. The probe may be either DNA or protein,
25 including an antibody.

EXAMPLES

The following experimental section and examples are offered by way of illustration and not by way of limitation.

30

I. Drosophila p53 screen

The Drosophila p53 gene (Ollmann M, et al., Cell 2000 101: 91-101) was overexpressed specifically in the wing using the vestigial margin quadrant enhancer. Increasing quantities of Drosophila p53 (titrated using different strength transgenic inserts

in 1 or 2 copies) caused deterioration of normal wing morphology from mild to strong, with phenotypes including disruption of pattern and polarity of wing hairs, shortening and thickening of wing veins, progressive crumpling of the wing and appearance of dark "death" inclusions in wing blade. In a screen designed to identify enhancers and
5 suppressors of Drosophila p53, homozygous females carrying two copies of p53 were crossed to 5663 males carrying random insertions of a piggyBac transposon (Fraser M *et al.*, *Virology* (1985) 145:356-361). Progeny containing insertions were compared to non-insertion-bearing sibling progeny for enhancement or suppression of the p53 phenotypes. Sequence information surrounding the piggyBac insertion site was used to identify the
10 modifier genes. Modifiers of the wing phenotype were identified as members of the p53 pathway.

II. Drosophila p21 screen

A dominant loss of function screen was carried out in *Drosophila* to identify genes
15 that interact with the cyclin dependent kinase inhibitor, p21 (Bourne HR, *et al.*, *Nature* (1990) 348(6297):125-132; Marshall CJ, *Trends Genet* (1991) 7(3):91-95). Expression of the p21 gene from GMR-p21 transgene (Hay, B. A., *et al.* (1994) *Development* 120:2121-2129) in the eye causes deterioration of normal eye morphology, resulting in reduced, rough eyes. Flies carrying this transgene were maintained as a stock (P 1025 F, genotype:
20 y w; P{p21-pExp-gl-w[+]Hsp70(3'UTR)-5}). Females of this stock were crossed to a collection of males carrying piggyBac insertions (Fraser M *et al.*, *Virology* (1985) 145:356-361). Resulting progeny carrying both the transgene and transposons were scored for the effect of the transposon on the eye phenotype, i.e. whether the transposon enhanced or suppressed (or had no effect) the eye phenotype. All data was recorded and
25 all modifiers were retested with a repeat of the original cross, and the retests were scored at least twice. Modifiers of the eye phenotype were identified as members of the p21 pathway.

III. Drosophila branching morphogenesis screen

30 Genetic screens were designed to identify modifiers of branching morphogenesis in *Drosophila*. Briefly, *Drosophila* embryos (approximately stage 16) that were homozygous for lethal insertions of a piggyBac (Fraser M *et al.*, *Virology* (1985) 145:356-361) or P-element transposon were screened for tracheal defects using monoclonal antibody 2A12 (Samakovlis C, *et al.*, *Development* (1996) 122:1395-1407; Patel NH.

(1994) Practical Uses in Cell and Molecular Biology. Eds LSB Goldstein and EA Fryberg. Vol 44 pp446-488. San Diego Academic Press). Sequence information surrounding the transposon insertion site was used to identify the gene mutated by the insertion.

5 IV. Analysis of Table 1

BLAST analysis (Altschul et al., *supra*) was employed to identify Targets from *Drosophila* modifiers. The columns "WHN symbol", and "WHN name aliases" provide a symbol and the known name abbreviations for the Targets, where available, from Genbank. "WHN RefSeq_NA or GI_NA", "WHN GI_AA", "WHN NAME", and "WHN Description" provide the reference DNA sequences for the WHNs as available from National Center for Biology Information (NCBI), WHN protein Genbank identifier number (GI#), WHN name, and WHN description, all available from Genbank, respectively. The length of each amino acid is in the "WHN Protein Length" column.

Names and Protein sequences of *Drosophila* modifiers of p21, p53, or branching morphogenesis from screens (Examples I, 2, 3), are represented in the "Modifier Name" and "Modifier GI_AA" column by GI#, respectively.

Table 1

WHN symbol	WHN RefSeq_na: Locus Link	NA SEQ ID NO:	WHN gi_aa	AA SEQ ID NO:	WHN name (Locus Link)	WHN Description	WHN Protein length	Modifier	Modifier gi_aa
WHN	NM_003593.2	1	182019134		winged-helix nude	Winged-helix nude, member of forkhead winged-helix transcription factor family, regulates transcription of hair keratin genes Ha3 II (KRTHA3B) and Hb5 (KRTH5B); mutation in the corresponding gene causes severe immunodeficiency and congenital alopecia	648	jumu	17737881

FOXN4	16506786	2	165067875	forkhead/winged helix transcription factor FOXN4	Protein containing a fork head domain, has low similarity to hepatocyte nuclear factor 3-gamma (mouse Foxa3), which regulates transcription of liver-specific genes and functions in endoderm development	448	jumu	17737881
LOC143958	20560710	3	205607116	similar to forkhead/winged helix transcription factor FOXN4	na	238	jumu	17737881

V. High-Throughput In Vitro Fluorescence Polarization Assay

Fluorescently-labeled WHN peptide/substrate are added to each well of a 96-well microtiter plate, along with a test agent in a test buffer (10 mM HEPES, 10 mM NaCl, 6 mM magnesium chloride, pH 7.6). Changes in fluorescence polarization, determined by using a Fluorolite FPM-2 Fluorescence Polarization Microtiter System (Dynatech Laboratories, Inc), relative to control values indicates the test compound is a candidate modifier of WHN activity.

10 VI. High-Throughput In Vitro Binding Assay.

³³P-labeled WHN peptide is added in an assay buffer (100 mM KCl, 20 mM HEPES pH 7.6, 1 mM MgCl₂, 1% glycerol, 0.5% NP-40, 50 mM beta-mercaptoethanol, 1 mg/ml BSA, cocktail of protease inhibitors) along with a test agent to the wells of a Neutralite-avidin coated assay plate and incubated at 25°C for 1 hour. Biotinylated substrate is then added to each well and incubated for 1 hour. Reactions are stopped by washing with PBS, and counted in a scintillation counter. Test agents that cause a difference in activity relative to control without test agent are identified as candidate p21, p53, or branching morphogenesis modulating agents.

20 VII. Immunoprecipitations and Immunoblotting

For coprecipitation of transfected proteins, 3 × 10⁶ appropriate recombinant cells containing the WHN proteins are plated on 10-cm dishes and transfected on the following

day with expression constructs. The total amount of DNA is kept constant in each transfection by adding empty vector. After 24 h, cells are collected, washed once with phosphate-buffered saline and lysed for 20 min on ice in 1 ml of lysis buffer containing 50 mM Hepes, pH 7.9, 250 mM NaCl, 20 mM -glycerophosphate, 1 mM sodium

5 orthovanadate, 5 mM p-nitrophenyl phosphate, 2 mM dithiothreitol, protease inhibitors (complete, Roche Molecular Biochemicals), and 1% Nonidet P-40. Cellular debris is removed by centrifugation twice at 15,000 × g for 15 min. The cell lysate is incubated with 25 µl of M2 beads (Sigma) for 2 h at 4 °C with gentle rocking.

10 After extensive washing with lysis buffer, proteins bound to the beads are solubilized by boiling in SDS sample buffer, fractionated by SDS-polyacrylamide gel electrophoresis, transferred to polyvinylidene difluoride membrane and blotted with the indicated antibodies. The reactive bands are visualized with horseradish peroxidase coupled to the appropriate secondary antibodies and the enhanced chemiluminescence (ECL) Western blotting detection system (Amersham Pharmacia Biotech).

15

VIII. Expression analysis

All cell lines used in the following experiments are NCI (National Cancer Institute) lines, and are available from ATCC (American Type Culture Collection, Manassas, VA 20110-2209). Normal and tumor tissues are obtained from Impath, UC Davis, Clontech, 20 Stratagene, and Ambion.

TaqMan analysis is used to assess expression levels of the disclosed genes in various samples.

RNA is extracted from each tissue sample using Qiagen (Valencia, CA) RNeasy kits, following manufacturer's protocols, to a final concentration of 50ng/µl. Single 25 stranded cDNA is then synthesized by reverse transcribing the RNA samples using random hexamers and 500ng of total RNA per reaction, following protocol 4304965 of Applied Biosystems (Foster City, CA).

Primers for expression analysis using TaqMan assay (Applied Biosystems, Foster City, CA) are prepared according to the TaqMan protocols, and the following criteria: a) 30 primer pairs are designed to span introns to eliminate genomic contamination, and b) each primer pair produced only one product.

Taqman reactions are carried out following manufacturer's protocols, in 25 µl total volume for 96-well plates and 10 µl total volume for 384-well plates, using 300nM primer and 250 nM probe, and approximately 25ng of cDNA. The standard curve for result

analysis is prepared using a universal pool of human cDNA samples, which is a mixture of cDNAs from a wide variety of tissues so that the chance that a target will be present in appreciable amounts is good. The raw data are normalized using 18S rRNA (universally expressed in all tissues and cells).

5 For each expression analysis, tumor tissue samples are compared with matched normal tissues from the same patient. A gene is considered overexpressed in a tumor when the level of expression of the gene is 2 fold or higher in the tumor compared with its matched normal sample. In cases where normal tissue is not available, a universal pool of cDNA samples is used instead. In these cases, a gene is considered overexpressed in a
10 tumor sample when the difference of expression levels between a tumor sample and the average of all normal samples from the same tissue type is greater than 2 times the standard deviation of all normal samples (i.e., Tumor – average(all normal samples) > 2 x STDEV(all normal samples)).

A modulator identified by an assay described herein can be further validated for
15 therapeutic effect by administration to a tumor in which the gene is overexpressed. A decrease in tumor growth confirms therapeutic utility of the modulator. Prior to treating a patient with the modulator, the likelihood that the patient will respond to treatment can be diagnosed by obtaining a tumor sample from the patient, and assaying for expression of the gene targeted by the modulator. The expression data for the gene(s) can also be used
20 as a diagnostic marker for disease progression. The assay can be performed by expression analysis as described above, by antibody directed to the gene target, or by any other available detection method.

WHAT IS CLAIMED IS:

1. A method of identifying a candidate p21, p53, or branching morphogenesis pathway modulating agent, said method comprising the steps of:
 - 5 (a) providing an assay system comprising a purified WHN polypeptide or nucleic acid or a functionally active fragment or derivative thereof;
 - (b) contacting the assay system with a test agent under conditions whereby, but for the presence of the test agent, the system provides a reference activity; and
 - (c) detecting a test agent-biased activity of the assay system, wherein a difference 10 between the test agent-biased activity and the reference activity identifies the test agent as a candidate p21, p53, or branching morphogenesis pathway modulating agent.
2. The method of Claim 1 wherein the assay system comprises cultured cells that express the WHN polypeptide.
 - 15 3. The method of Claim 2 wherein the cultured cells additionally have defective p21, p53, or branching morphogenesis function.
 4. The method of Claim 1 wherein the assay system includes a screening assay 20 comprising a WHN polypeptide, and the candidate test agent is a small molecule modulator.
 5. The method of Claim 4 wherein the assay is a binding assay.
- 25 6. The method of Claim 1 wherein the assay system is selected from the group consisting of an apoptosis assay system, a cell proliferation assay system, an angiogenesis assay system, a cell migration assay system, a tubulogenesis assay system, a sprouting assay system, and a hypoxic induction assay system.
- 30 7. The method of Claim 1 wherein the assay system includes a binding assay comprising a WHN polypeptide and the candidate test agent is an antibody.
8. The method of Claim 1 wherein the assay system includes an expression assay comprising a WHN nucleic acid and the candidate test agent is a nucleic acid modulator.

9. The method of Claim 8 wherein the nucleic acid modulator is an antisense oligomer.

10. The method of Claim 8 wherein the nucleic acid modulator is a PMO.

5

11. The method of Claim 1 additionally comprising:

(d) administering the candidate p21, p53, or branching morphogenesis pathway modulating agent identified in (c) to a model system comprising cells defective in p21, p53, or branching morphogenesis function and, detecting a phenotypic change in the
10 model system that indicates that the p21, p53, or branching morphogenesis function is restored.

12. The method of Claim 11 wherein the model system is a mouse model with defective p21, p53, or branching morphogenesis function.

15

13. A method for modulating a p21, p53, or branching morphogenesis pathway of a cell comprising contacting a cell defective in p21, p53, or branching morphogenesis function with a candidate modulator that specifically binds to a WHN polypeptide, whereby p21, p53, or branching morphogenesis function is restored.

20

14. The method of Claim 13 wherein the candidate modulator is administered to a vertebrate animal predetermined to have a disease or disorder resulting from a defect in p21, p53, or branching morphogenesis function.

25

15. The method of Claim 13 wherein the candidate modulator is selected from the group consisting of an antibody and a small molecule.

16. The method of Claim 1, comprising the additional steps of:

(e) providing a secondary assay system comprising cultured cells or a non-human
30 animal expressing WHN ,
(f) contacting the secondary assay system with the test agent of (b) or an agent derived therefrom under conditions whereby, but for the presence of the test agent or agent derived therefrom, the system provides a reference activity; and
(g) detecting an agent-biased activity of the second assay system,

wherein a difference between the agent-biased activity and the reference activity of the second assay system confirms the test agent or agent derived therefrom as a candidate p21, p53, or branching morphogenesis pathway modulating agent,

and wherein the second assay detects an agent-biased change in the p21, p53, or
5 branching morphogenesis pathway.

17. The method of Claim 16 wherein the secondary assay system comprises cultured cells.

10 18. The method of Claim 16 wherein the secondary assay system comprises a non-human animal.

19. The method of Claim 18 wherein the non-human animal mis-expresses a p21, p53, or branching morphogenesis pathway gene.

15 20. A method of modulating p21, p53, or branching morphogenesis pathway in a mammalian cell comprising contacting the cell with an agent that specifically binds a WHN polypeptide or nucleic acid.

20 21. The method of Claim 20 wherein the agent is administered to a mammalian animal predetermined to have a pathology associated with the p21, p53, or branching morphogenesis pathway.

22. The method of Claim 20 wherein the agent is a small molecule modulator, a nucleic acid modulator, or an antibody.

25

23. A method for diagnosing a disease in a patient comprising:

(a) obtaining a biological sample from the patient;
(b) contacting the sample with a probe for WHN expression;
30 (c) comparing results from step (b) with a control;
(d) determining whether step (c) indicates a likelihood of disease.

24. The method of claim 23 wherein said disease is cancer.

SEQUENCE LISTING

<110> EXELIXIS, INC.

<120> WHNs AS MODIFIERS OF p53, p21, AND BRANCHING MORPHOGENESIS PATHWAYS AND METHODS OF USE

<130> EX03-063C-PC

<150> US 60/411,152

<151> 2002-09-16

<160> 6

<170> PatentIn version 3.2

<210> 1

<211> 2697

<212> DNA

<213> Homo sapiens

<400> 1

acggctttct ttgaggccag gactgggtga tggtgtcgct acccccgcgg cagtctgacg	60
tcacgctgcc gggccccacc agactggagg gcgagcgcca aggggacctc atgcaggcac	120
cgggcctccc aggctccctt gccccacaga gtaagcatgc cggcttcagc tgctcgatcat	180
ttgtgtccga cggccctcca gagaggacac cctcaactgcc cccacacagc cccgcattt	240
cgtcaccagg gcccggcaaa gtccaggggcc actgcccagc cggcccccggc cctggggccct	300
tcaggctctc accctcagac aagtatcctt gctttggctt tgaggaggcc gcagcaagca	360
gccctgggcg attcctcaag ggcagccacg cggcccttcca cccgtacaag cggcctttcc	420
atgaggacgt ctcccagag gccgagacca ccctggccct caaaggacac tcctttaaga	480
ccccaggggcc gctggaggcc ttggaggaga tcccagtggc cgtggggag gccggccct	540
tcctgcctgg ctctcagca gaggctgggt gtaacgggct cccctacccc agccaggagc	600
atggcccccata agtcctgggt tcagaggtca aagtcaagcc cccagttctg gagagtggtg	660
ctggatgtt ctgctaccag cctcccttgc agcatatgta ctgctcccttcc cagccccctt	720
tccaccagta ctcgccaggt ggtggcagct accccataacc ctacctgggc tcctcacact	780
atcagtacca gcgaatggca ccccaggcca gcaccgatgg gcaccggcct ctcttcccaa	840
aaccatcta ttcctacagc atcctcatct tcatggccct taagaacagt aaaactggaa	900
gccttccctgt cagcgagatc tacaattttt tgacggagca ctttccttac ttcaagacag	960
cacccgatgg ctggagaat tctgtccggc acaacctatc cctcaacaag tgcttcgaga	1020
aggtggagaa caaatcagga agttccccc gcaagggtcg cctgtggggcc ctcaatccgg	1080
ccaagatcga caagatgcaa gaggagctgc aaaaatggaa gagaaaaagat cccattgctg	1140
tgcgcaaaag catggccaag ccagaagagc tggacagcct cattggagac aagagagaaa	1200

agctgggctc cccactcctg ggctgtccgc cccctggct gtccggctca ggccccatcc 1260
 ggccctggc acccccagct ggcctctccc caccactgca ctcactccac ccagctccag 1320
 gccccattcc tggcaagaac cccctgcagg acctacttat ggggcacaca ccctcctgct 1380
 atggcagac atacttgac ctcctcaccag gcctggcccc tcctggaccc ccgcagccat 1440
 tgttcccaca gccggacggg caccttgagc tgccggccca gccaggcacc ccccaggact 1500
 cgcctctgcc tgcccacacc ccacccagcc acagtgc当地 gctactggcc gagccttccc 1560
 cagccaggac tatgcacgac accctgctgc cagatggaga ccttggcaact gacctggatg 1620
 ccatcaatcc ctcactcact gacttcgact tccagggaaa cctgtggaa cagttgaagg 1680
 atgatacgctt ggccctcgac cccctggta tggtgacccat atccccaca tcatcttcga 1740
 tgccaccacc ccagccacca cctcactgct tccccctgg gccctgtctg acagagacag 1800
 gcagtggggc aaggtaacttg gcagccccgg gcagtggta ctccggggca ctgggtgacc 1860
 tgcacccac caccctctac tctgcctta tggagctgga gcccacgccc cccacggccc 1920
 ctgcaggccc ctctgtgtac ctcagcccca gctccaagcc cgtggccctg gcatgagctg 1980
 tgccagctt cgtcagctcc agcggtgcc tggctggaa gtcctggccg gccgcccaca 2040
 tcgggctcac ottaaaggta aaggaaggaa aataactacat gtcccccata gcaactaagcc 2100
 aacgtgtgtc tcagctggtt gctggggcg cagaggacat cacctgggt gctgcctctc 2160
 acacatttct gccacgttgtt ggccagctc ctcacccagg gcccccaaag agcaagcgct 2220
 tggcaagag gaaaatgccc tgcccttagc tcacactcat ccacacttaa gccctcggtc 2280
 acacacacaa attattcaga tgtacaccca cccacatatac ttacagccag aggaaccagc 2340
 actccatcac tgagagcccg acttcgtttc tggggcaact gagagctgag cgcttgctt 2400
 accaaaagct cagggccctg tgccaggcca aagatcccc cagacccca ttctgacatc 2460
 cacatgctct gcagtcgtgg cccctcgctc atttcttcc ccagaagcgc cctgtattta 2520
 ttccccatc ttcatccaa cagccagca agaaggagga gacagagagc tcctccctgg 2580
 gttgtctgtc gaccccccga ggagctgcta attggcagca cccactcagc cattctctac 2640
 ccatccttag tacatgctct gtccagcttt ccccagggtg acatacagaa ggggcaa 2697

<210> 2
 <211> 1344
 <212> DNA
 <213> Homo sapiens

<400> 2
 ggggacctgc agtcgctgtc gtggctcacg gcgggtggatg tgccctcggtc gcagcagatg 60
 gcaagtggcc gcgtggacct ggggtggccca tgcgtgccac atccacaccc aggtgccttg 120
 gctgggggtgg ccgacctgca tgtgggagcc actccaaatgc cccttctcca tggcccagca 180

ggcatggccc cccgaggcat gccaggtctg ggccccataa ctggccacag agacagcatg	240
agccagttcc ccgtgggggg ccagccctca tctggcctgc aggaccggcc gcatctgtac	300
tcacctgccca cccaaaccaca gttcccgctc ccccccgggtg cccagcagtg ccctcctgtg	360
ggcctctatg gccccccatt tggggtgccg ccccccattacc cccagccccca cgtggctgtg	420
cattcatctc aagaactgca ccccaaacac taccccaagg ccattctactc gtacagctgt	480
ctgatcgcca tggccctgaa gaacagcaag acaggcagcc tgcctgtgag cgagatctac	540
agcttcatga aggagcactt cccctacttc aagacggccc ccgacgggtg gaagaactcg	600
gtgcggcaca acctgtctc gaacaagtgc ttgcagaagg tggagaacaa gatgagcggc	660
tcctcccgca agggctgctt gtgggctctg aacctggccc gcatcgacaa gatggaggag	720
gagatgcaca agtggaaagag gaaggacctg gctgccatcc accggagtat ggccaaccct	780
gaggagttgg acaagctgat ctccgaccgg cctgaaaagct gccggcgccc cggcaaaccg	840
gggaaaccag aggccccctg gctgactcac gccaccacag tggccgtggc gcatggctgc	900
ctggctgtct cccagctccc accccagcca ctgatgaccc tgccttgca gtcagtc	960
ctgcaccacc aggtccagcc ccaggcacat cttgctccag actctccagc accagcccg	1020
acccggccac tgcacgccc gccggacctc agccccagcc cgctcccca cccggccatg	1080
ggaagggctc ctgttagactt catcaacatc agcaccgaca tgaacactga ggtggatgcc	1140
ctcgaccacc gcatcatgga cttcgctctg caggggaacc tgtgggagga gatgaaggat	1200
gagggattca gcttggacac actggcgcc tttgcagact ccccgcttgg ctgtgacctg	1260
ggggcctcag gcctaaccctc tgcctcggtt ggcagcgacc agtccttc agacttgca	1320
gtgacgggtc tctacacagc gtac	1344

<210> 3
 <211> 869
 <212> DNA
 <213> Homo sapiens

<400> 3	
ttgcaggta taaaactccga attgttaagc cacaaaaatt acccctagag aaaaaaccca	60
accctgataa ggttgtccca gattatgagc ccaacctctg gatgtggta aatcccaaca	120
tttgttatcc ccctggaaag ctggaggtct caggacgtag gaagagggag gacctgacaa	180
gcacactccc ctccctctcag ccacccaga aggaggaaga tgccagctgc tcagaggccg	240
caggggtgga atcaactgtcc cagtcctcca gcaagcggtc tccccctcgg aagcggtttg	300
ccttttcccc cagcacctgg gagctcacag aagaggagga ggctgaggac caggaagaca	360
gctcctctat ggctctccca tcccctcaca aaagggcccc cctccagagt cgaggccttc	420

ggcaagccag cagccaggcg gggaggctct ggtcccgccc ccctctaat tacttccacc	480
taattgccct ggcattaaga aacagttccc cctgtggcct caacgtgcaa cagatctaca	540
gtttcactcg aaagcacttc cccttttcc ggacggcccc ggaaggctgg aagaatactg	600
tccgtcacaa tctctgtttt cgagacagct ttgagaaaagt gcctgtcagc atgcagggcg	660
ggccagcac acggcctcga tcttgccct ggaagttgac cgaggaggga caccggcgct	720
ttgcggagga ggcccgccgc ttggcttcca ctcggctaga aagtatccaa cagtgcatga	780
gccagccaga tgtgatgccc ttccctttt atcttaacc ccaagaagca acagccagct	840
aatgcttat taaaattacc ctcactagc	869

<210> 4

<211> 648

<212> PRT

<213> Homo sapiens

<400> 4

Met Val Ser Leu Pro Pro Pro Gln Ser Asp Val Thr Leu Pro Gly Pro			
1	5	10	15

Thr Arg Leu Glu Gly Glu Arg Gln Gly Asp Leu Met Gln Ala Pro Gly			
20	25	30	

Leu Pro Gly Ser Pro Ala Pro Gln Ser Lys His Ala Gly Phe Ser Cys			
35	40	45	

Ser Ser Phe Val Ser Asp Gly Pro Pro Glu Arg Thr Pro Ser Leu Pro			
50	55	60	

Pro His Ser Pro Arg Ile Ala Ser Pro Gly Pro Glu Gln Val Gln Gly			
65	70	75	80

His Cys Pro Ala Gly Pro Gly Pro Phe Arg Leu Ser Pro Ser			
85	90	95	

Asp Lys Tyr Pro Gly Phe Gly Phe Glu Ala Ala Ala Ser Ser Pro			
100	105	110	

Gly Arg Phe Leu Lys Gly Ser His Ala Pro Phe His Pro Tyr Lys Arg			
115	120	125	

Pro Phe His Glu Asp Val Phe Pro Glu Ala Glu Thr Thr Leu Ala Leu			
130	135	140	

Lys Gly His Ser Phe Lys Thr Pro Gly Pro Leu Glu Ala Phe Glu Glu			
145	150	155	160

Ile Pro Val Asp Val Ala Glu Ala Glu Ala Phe Leu Pro Gly Phe Ser
165 170 175

Ala Glu Ala Trp Cys Asn Gly Leu Pro Tyr Pro Ser Gln Glu His Gly
180 185 190

Pro Gln Val Leu Gly Ser Glu Val Lys Val Lys Pro Pro Val Leu Glu
195 200 205

Ser Gly Ala Gly Met Phe Cys Tyr Gln Pro Pro Leu Gln His Met Tyr
210 215 220

Cys Ser Ser Gln Pro Pro Phe His Gln Tyr Ser Pro Gly Gly Ser
225 230 235 240

Tyr Pro Ile Pro Tyr Leu Gly Ser Ser His Tyr Gln Tyr Gln Arg Met
245 250 255

Ala Pro Gln Ala Ser Thr Asp Gly His Gln Pro Leu Phe Pro Lys Pro
260 265 270

Ile Tyr Ser Tyr Ser Ile Leu Ile Phe Met Ala Leu Lys Asn Ser Lys
275 280 285

Thr Gly Ser Leu Pro Val Ser Glu Ile Tyr Asn Phe Met Thr Glu His
290 295 300

Phe Pro Tyr Phe Lys Thr Ala Pro Asp Gly Trp Lys Asn Ser Val Arg
305 310 315 320

His Asn Leu Ser Leu Asn Lys Cys Phe Glu Lys Val Glu Asn Lys Ser
325 330 335

Gly Ser Ser Ser Arg Lys Gly Cys Leu Trp Ala Leu Asn Pro Ala Lys
340 345 350

Ile Asp Lys Met Gln Glu Glu Leu Gln Lys Trp Lys Arg Lys Asp Pro
355 360 365

Ile Ala Val Arg Lys Ser Met Ala Lys Pro Glu Glu Leu Asp Ser Leu
370 375 380

Ile Gly Asp Lys Arg Glu Lys Leu Gly Ser Pro Leu Leu Gly Cys Pro
385 390 395 400

Pro Pro Gly Leu Ser Gly Ser Gly Pro Ile Arg Pro Leu Ala Pro Pro
405 410 415

Ala Gly Leu Ser Pro Pro Leu His Ser Leu His Pro Ala Pro Gly Pro
420 425 430

Ile Pro Gly Lys Asn Pro Leu Gln Asp Leu Leu Met Gly His Thr Pro
435 440 445

Ser Cys Tyr Gly Gln Thr Tyr Leu His Leu Ser Pro Gly Leu Ala Pro
450 455 460

Pro Gly Pro Pro Gln Pro Leu Phe Pro Gln Pro Asp Gly His Leu Glu
465 470 475 480

Leu Arg Ala Gln Pro Gly Thr Pro Gln Asp Ser Pro Leu Pro Ala His
485 490 495

Thr Pro Pro Ser His Ser Ala Lys Leu Leu Ala Glu Pro Ser Pro Ala
500 505 510

Arg Thr Met His Asp Thr Leu Leu Pro Asp Gly Asp Leu Gly Thr Asp
515 520 525

Leu Asp Ala Ile Asn Pro Ser Leu Thr Asp Phe Asp Phe Gln Gly Asn
530 535 540

Leu Trp Glu Gln Leu Lys Asp Asp Ser Leu Ala Leu Asp Pro Leu Val
545 550 555 560

Leu Val Thr Ser Ser Pro Thr Ser Ser Met Pro Pro Pro Gln Pro
565 570 575

Pro Pro His Cys Phe Pro Pro Gly Pro Cys Leu Thr Glu Thr Gly Ser
580 585 590

Gly Ala Gly Asp Leu Ala Ala Pro Gly Ser Gly Gly Ser Gly Ala Leu
595 600 605

Gly Asp Leu His Leu Thr Thr Leu Tyr Ser Ala Phe Met Glu Leu Glu
610 615 620

Pro Thr Pro Pro Thr Ala Pro Ala Gly Pro Ser Val Tyr Leu Ser Pro
625 630 635 640

Ser Ser Lys Pro Val Ala Leu Ala
645

<210> 5
<211> 448
<212> PRT
<213> Homo sapiens

<400> 5

Gly Asp Leu Gln Ser Leu Ser Trp Leu Thr Ala Val Asp Val Pro Arg
1 5 10 15

Leu Gln Gln Met Ala Ser Gly Arg Val Asp Leu Gly Gly Pro Cys Val
20 25 30

Pro His Pro His Pro Gly Ala Leu Ala Gly Val Ala Asp Leu His Val
35 40 45

Gly Ala Thr Pro Ser Pro Leu Leu His Gly Pro Ala Gly Met Ala Pro
50 55 60

Arg Gly Met Pro Gly Leu Gly Pro Ile Thr Gly His Arg Asp Ser Met
65 70 75 80

Ser Gln Phe Pro Val Gly Gly Gln Pro Ser Ser Gly Leu Gln Asp Pro
85 90 95

Pro His Leu Tyr Ser Pro Ala Thr Gln Pro Gln Phe Pro Leu Pro Pro
100 105 110

Gly Ala Gln Gln Cys Pro Pro Val Gly Leu Tyr Gly Pro Pro Phe Gly
115 120 125

Val Arg Pro Pro Tyr Pro Gln Pro His Val Ala Val His Ser Ser Gln
130 135 140

Glu Leu His Pro Lys His Tyr Pro Lys Pro Ile Tyr Ser Tyr Ser Cys
145 150 155 160

Leu Ile Ala Met Ala Leu Lys Asn Ser Lys Thr Gly Ser Leu Pro Val
165 170 175

Ser Glu Ile Tyr Ser Phe Met Lys Glu His Phe Pro Tyr Phe Lys Thr
180 185 190

Ala Pro Asp Gly Trp Lys Asn Ser Val Arg His Asn Leu Ser Leu Asn
195 200 205

Lys Cys Phe Glu Lys Val Glu Asn Lys Met Ser Gly Ser Ser Arg Lys

210

215

220

Gly Cys Leu Trp Ala Leu Asn Leu Ala Arg Ile Asp Lys Met Glu Glu
225 230 235 240

Glu Met His Lys Trp Lys Arg Lys Asp Leu Ala Ala Ile His Arg Ser
245 250 255

Met Ala Asn Pro Glu Glu Leu Asp Lys Leu Ile Ser Asp Arg Pro Glu
260 265 270

Ser Cys Arg Arg Pro Gly Lys Pro Gly Glu Pro Glu Ala Pro Val Leu
275 280 285

Thr His Ala Thr Thr Val Ala Val Ala His Gly Cys Leu Ala Val Ser
290 295 300

Gln Leu Pro Pro Gln Pro Leu Met Thr Leu Ser Leu Gln Ser Val Pro
305 310 315 320

Leu His His Gln Val Gln Pro Gln Ala His Leu Ala Pro Asp Ser Pro
325 330 335

Ala Pro Ala Gln Thr Pro Pro Leu His Ala Leu Pro Asp Leu Ser Pro
340 345 350

Ser Pro Leu Pro His Pro Ala Met Gly Arg Ala Pro Val Asp Phe Ile
355 360 365

Asn Ile Ser Thr Asp Met Asn Thr Glu Val Asp Ala Leu Asp Pro Ser
370 375 380

Ile Met Asp Phe Ala Leu Gln Gly Asn Leu Trp Glu Glu Met Lys Asp
385 390 395 400

Glu Gly Phe Ser Leu Asp Thr Leu Gly Ala Phe Ala Asp Ser Pro Leu
405 410 415

Gly Cys Asp Leu Gly Ala Ser Gly Leu Thr Pro Ala Ser Gly Gly Ser
420 425 430

Asp Gln Ser Phe Pro Asp Leu Gln Val Thr Gly Leu Tyr Thr Ala Tyr
435 440 445

<210> 6
<211> 238
<212> PRT

<213> Homo sapiens

<400> 6

Met Trp Val Asn Pro Asn Ile Val Tyr Pro Pro Gly Lys Leu Glu Val
1 5 10 15

Ser Gly Arg Arg Lys Arg Glu Asp Leu Thr Ser Thr Leu Pro Ser Ser
20 25 30

Gln Pro Pro Gln Lys Glu Glu Asp Ala Ser Cys Ser Glu Ala Ala Gly
35 40 45

Val Glu Ser Leu Ser Gln Ser Ser Ser Lys Arg Ser Pro Pro Arg Lys
50 55 60

Arg Phe Ala Phe Ser Pro Ser Thr Trp Glu Leu Thr Glu Glu Glu Glu
65 70 75 80

Ala Glu Asp Gln Glu Asp Ser Ser Ser Met Ala Leu Pro Ser Pro His
85 90 95

Lys Arg Ala Pro Leu Gln Ser Arg Arg Leu Arg Gln Ala Ser Ser Gln
100 105 110

Ala Gly Arg Leu Trp Ser Arg Pro Pro Leu Asn Tyr Phe His Leu Ile
115 120 125

Ala Leu Ala Leu Arg Asn Ser Ser Pro Cys Gly Leu Asn Val Gln Gln
130 135 140

Ile Tyr Ser Phe Thr Arg Lys His Phe Pro Phe Phe Arg Thr Ala Pro
145 150 155 160

Glu Gly Trp Lys Asn Thr Val Arg His Asn Leu Cys Phe Arg Asp Ser
165 170 175

Phe Glu Lys Val Pro Val Ser Met Gln Gly Gly Ala Ser Thr Arg Pro
180 185 190

Arg Ser Cys Leu Trp Lys Leu Thr Glu Glu Gly His Arg Arg Phe Ala
195 200 205

Glu Glu Ala Arg Ala Leu Ala Ser Thr Arg Leu Glu Ser Ile Gln Gln
210 215 220

Cys Met Ser Gln Pro Asp Val Met Pro Phe Leu Phe Asp Leu
225 230 235